

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:17:19 ; Search time 19 Seconds
(without alignments)
16.303 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	236	4	US-09-632-570-17 Sequence 17, Appl
2	37	92.5	236	4	US-09-632-575-47 Sequence 47, Appl
3	37	92.5	938	4	US-09-252-991A-23882 Sequence 23882, A
4	36	90.0	68	4	US-09-252-991A-18367 Sequence 18367, A
5	36	90.0	142	4	US-09-252-991A-31533 Sequence 31533, A
6	36	90.0	174	4	US-09-325-932A-163 Sequence 163, App
7	36	90.0	225	4	US-09-325-932A-162 Sequence 162, App
8	36	90.0	242	4	US-09-345-936B-3 Sequence 3, Appli
9	36	90.0	378	4	US-09-325-932A-158 Sequence 158, App
10	36	90.0	445	4	US-09-252-991A-22368 Sequence 22368, A
11	36	90.0	462	4	US-09-252-991A-21704 Sequence 21704, A
12	34	85.0	44	3	US-08-905-223-274 Sequence 274, App
13	33	82.5	74	1	US-08-379-538-2 Sequence 2, Appli
14	33	82.5	136	2	US-08-774-065-2 Sequence 2, Appli
15	33	82.5	164	4	US-09-252-991A-23817 Sequence 23817, A
16	33	82.5	218	1	US-08-032-848C-10 Sequence 10, Appl
17	33	82.5	218	1	US-08-438-870-10 Sequence 10, Appl
18	33	82.5	218	2	US-08-169-948B-34 Sequence 34, Appl
19	33	82.5	218	2	US-08-448-873-34 Sequence 34, Appl
20	33	82.5	218	3	US-08-382-452D-34 Sequence 34, Appl
21	33	82.5	218	3	US-09-216-295-1 Sequence 1, Appli
22	33	82.5	218	4	US-08-507-362A-18 Sequence 18, Appl
23	33	82.5	218	4	US-09-916-494A-34 Sequence 34, Appl
24	33	82.5	218	4	US-09-632-570-1 Sequence 1, Appli
25	33	82.5	218	4	US-09-632-575-31 Sequence 31, Appl
26	33	82.5	232	3	US-09-146-770-1 Sequence 1, Appli
27	33	82.5	232	4	US-09-633-084-1 Sequence 1, Appli

28	33	82.5	232	4	US-10-075-872-1	Sequence 1, Appli
29	33	82.5	232	4	US-10-261-997-1	Sequence 1, Appli
30	33	82.5	234	1	US-08-032-848C-9	Sequence 9, Appli
31	33	82.5	234	1	US-08-438-870-9	Sequence 9, Appli
32	33	82.5	234	3	US-09-146-770-3	Sequence 3, Appli
33	33	82.5	234	3	US-09-146-770-4	Sequence 4, Appli
34	33	82.5	234	3	US-09-216-295-3	Sequence 3, Appli
35	33	82.5	234	3	US-09-216-295-4	Sequence 4, Appli
36	33	82.5	234	4	US-09-633-084-3	Sequence 3, Appli
37	33	82.5	234	4	US-09-633-084-4	Sequence 4, Appli
38	33	82.5	234	4	US-10-075-872-3	Sequence 3, Appli
39	33	82.5	234	4	US-10-075-872-4	Sequence 4, Appli
40	33	82.5	234	4	US-10-261-997-3	Sequence 3, Appli
41	33	82.5	234	4	US-10-261-997-4	Sequence 4, Appli
42	33	82.5	234	4	US-09-632-570-3	Sequence 3, Appli
43	33	82.5	234	4	US-09-632-570-4	Sequence 4, Appli
44	33	82.5	234	4	US-09-632-575-33	Sequence 33, Appl
45	33	82.5	234	4	US-09-632-575-34	Sequence 34, Appl
46	33	82.5	238	4	US-09-632-570-15	Sequence 15, Appl
47	33	82.5	238	4	US-09-632-575-45	Sequence 45, Appl
48	33	82.5	239	3	US-09-216-295-15	Sequence 15, Appl
49	33	82.5	316	4	US-09-252-991A-17312	Sequence 17312, A
50	33	82.5	467	1	US-08-140-104A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-632-570-17
; Sequence 17, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-570-17

Query Match 92.5%; Score 37; DB 4; Length 236;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 63 ADWSWS 68

RESULT 2
US-09-632-575-47
; Sequence 47, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0


```
; SEQ ID NO 47
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-575-47

Query Match          92.5%; Score 37; DB 4; Length 236;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      63 ADWSWS 68

RESULT 3
US-09-252-991A-23882
; Sequence 23882, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23882
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23882

Query Match          92.5%; Score 37; DB 4; Length 938;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      581 ADAWAWA 586

RESULT 4
US-09-252-991A-18367
; Sequence 18367, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18367
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367

Query Match          90.0%; Score 36; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
```

```
Db      2 DWSWA 6

RESULT 5
US-09-252-991A-31533
; Sequence 31533, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31533
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533

Query Match          90.0%; Score 36; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      94 ADWSW 98

RESULT 6
US-09-325-932A-163
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163

Query Match          90.0%; Score 36; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      109 ADWSW 113

RESULT 7
US-09-325-932A-162
; Sequence 162, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
```


FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 162
LENGTH: 225
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 100 ADWSW 104

RESULT 8
US-09-345-236B-3
Sequence 3, Application US/09345236B
Patent No. 6521454
GENERAL INFORMATION:

APPLICANT: Becnel, James J.
APPLICANT: Tuku, Fukuda
APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.0004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: mosquito baculovirus
US-09-345-236B-3

Query Match 90.0%; Score 36; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 80 DWSWA 84

RESULT 9
US-09-325-932A-158
Sequence 158, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develop
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 158
LENGTH: 378
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 128 ADWSW 132

RESULT 10
US-09-252-991A-22368
Sequence 22368, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22368
LENGTH: 445
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22368

Query Match 90.0%; Score 36; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 304 DWSWA 308

RESULT 11
US-09-252-991A-21704
Sequence 21704, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21704
LENGTH: 462
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 169 DWSWA 173

RESULT 12
US-08-905-223-274

; Sequence 274, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 274:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -26..-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 9.6
; OTHER INFORMATION: seq WLIALASWSWALC/RI
US-08-905-223-274

Query Match 85.0%; Score 34; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 19 ASWSWA 24

RESULT 13
US-08-379-538-2
; Sequence 2, Application US/08379538
; Patent No. 5804554
; GENERAL INFORMATION:
; APPLICANT: Volkmann, Robert A.
; APPLICANT: Saccomano, Nicholas A.
; APPLICANT: Nason II, Deane M.
; APPLICANT: Heck, Steven D.
; APPLICANT: Ronau, Robert T.
; TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
; TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pfizer Inc
; STREET: 235 East 42nd Street

; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,538
; FILING DATE: 3-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/887073
; FILING DATE: 21-MAY-1992
; APPLICATION NUMBER: PCT/US93/03921
; FILING DATE: 30-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Zielinski, Bryan
; REGISTRATION NUMBER: 34,462
; REFERENCE/DOCKET NUMBER: PC8175A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 573-4585
; TELEFAX: (212) 573-1939
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Filistata hibernalis
; TISSUE TYPE: venom
US-08-379-538-2

Query Match 82.5%; Score 33; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 52 DWSWS 56

RESULT 14
US-08-774-065-2
; Sequence 2, Application US/08774065
; Patent No. 5989899
; GENERAL INFORMATION:
; APPLICANT: Bower, Benjamin
; APPLICANT: Clarkson, Kathleen
; APPLICANT: Larenas, Edmund
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS
; TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND
; TITLE OF INVENTION: IN THE TREATMENT OF TEXTILES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL
; STREET: 925 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,065
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J.
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-846-7620
; TELEFAX: 415-845-6504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-774-065-2

Query Match 82.5%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 62 ADWQWS 67

RESULT 15

US-09-252-991A-23817
; Sequence 23817, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23817
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23817

Query Match 82.5%; Score 33; DB 4; Length 164;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 132 AGWSWA 137

RESULT 16

US-08-032-848C-10
; Sequence 10, Application US/08032848C
; Patent No. 5475101
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of
; TITLE OF INVENTION: EG III Cellulase

;
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/032,848C
; FILING DATE: MAR 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.
; REGISTRATION NUMBER: 33,401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7356
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-032-848C-10

Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 46 ADWQWS 51

RESULT 17

US-08-438-870-10
; Sequence 10, Application US/08438870
; Patent No. 5753484
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of EG
; TITLE OF INVENTION: III Cellulase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,870
; FILING DATE: May 10, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 35,696

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7555
TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-870-10

Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 46 ADWQWS 51

RESULT 18
US-08-169-948B-34
Sequence 34, Application US/08169948B
Patent No. 5861271
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen
APPLICANT: Collier, Katherine
APPLICANT: Larenas, Edmund
TITLE OF INVENTION: No. 5861271el Cellulase Enzymes and Systems
TITLE OF INVENTION: For Their Expression
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,948B
FILING DATE: DEC 17 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-169-948B-34

Query Match 82.5%; Score 33; DB 2; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 46 ADWQWS 51

RESULT 19
US-08-448-873-34
Sequence 34, Application US/08448873
Patent No. 5874276
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen
APPLICANT: Collier, Katherine A.
APPLICANT: Larenas, Edmund
TITLE OF INVENTION: No. 5874276el Cellulase Enzymes and Systems
TITLE OF INVENTION: For Their Expressions
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,873
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/169,948
FILING DATE: 17-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC226D14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-873-34

Query Match 82.5%; Score 33; DB 2; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 46 ADWQWS 51

RESULT 20
US-08-382-452D-34
Sequence 34, Application US/08382452D
Patent No. 6268196
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Ward, Michael
APPLICANT: Collier, Katherine D.
APPLICANT: Larenas, Edmund A.
TITLE OF INVENTION: NOVEL CELLULOSE ENZYMES AND SYSTEMS
TITLE OF INVENTION: FOR THEIR EXPRESSION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Genencor International
;; STREET: 925 Page Mill Road
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/382,452D
;; FILING DATE: February 1, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Christopher L. Stone
;; REGISTRATION NUMBER: 36,696
;; REFERENCE/DOCKET NUMBER: GC226-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 742-7555
;; TELEFAX: (415) 742-7217
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 218 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-382-452D-34

Query Match 82.5%; Score 33; DB 3; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 46 ADWQWS 51

RESULT 21
US-09-216-295-1
; Sequence 1, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328e1 Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Trichoderma longibrachiatum
US-09-216-295-1

Query Match 82.5%; Score 33; DB 3; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 46 ADWQWS 51

RESULT 22
US-08-507-362A-18
; Sequence 18, Application US/08507362A
; Patent No. 6562340
; GENERAL INFORMATION:
; APPLICANT: Bedford, Michael

;; Morgan, Andrew
;; Fowler, Timothy
;; Ward, Michael
;; Clarkson, Kathleen
;; Collier, Katherine
;; Larenas, Edmund
;;
;; TITLE OF INVENTION: An Enzyme Feed Additive and Animal Feed Including It
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genencor International
;; STREET: 925 Page Mill Road
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/507,362A
;; FILING DATE: 27-Oct-1995
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Castaneda, Janet
;; REGISTRATION NUMBER: 33,228
;; REFERENCE/DOCKET NUMBER: GC226-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 846-4072
;; TELEFAX: (650) 845-6504
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 218 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-507-362A-18

Query Match 82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |:
Db 46 ADWQWS 51

RESULT 23
US-09-916-494A-34
; Sequence 34, Application US/09916494A
; Patent No. 6620605
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Ward, Michael
; APPLICANT: Collier, Katherine D.
; APPLICANT: Larenas, Edmund
; TITLE OF INVENTION: Method and Compositions for Treating
; TITLE OF INVENTION: Cellulose Containing Fabrics Using Truncated Cellulase
; TITLE OF INVENTION: Enzyme Compositions
; FILE REFERENCE: GC226-C4
; CURRENT APPLICATION NUMBER: US/09/916,494A
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 08/382,452
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: US 08/169,948
; PRIOR FILING DATE: 1993-12-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34


```

;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Trichoderma longibrachiatum
US-09-916-494A-34

Query Match      82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||:
Db      46 ADWQWS 51

RESULT 24
US-09-632-570-1
; Sequence 1, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-09-632-570-1

Query Match      82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||:
Db      46 ADWQWS 51

RESULT 25
US-09-632-575-31
; Sequence 31, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-09-632-575-31

Query Match      82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||:
Db      46 ADWQWS 51
```

```

RESULT 26
US-09-146-770-1
; Sequence 1, Application US/09146770
; Patent No. 6187732
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/146,770
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-09-146-770-1

Query Match      82.5%; Score 33; DB 3; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||:
Db      60 ADWQWS 65

RESULT 27
US-09-633-084-1
; Sequence 1, Application US/09633084
; Patent No. 6407046
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/633,084
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/146,770
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-09-633-084-1

Query Match      82.5%; Score 33; DB 4; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||:
Db      60 ADWQWS 65

RESULT 28
US-10-075-872-1
; Sequence 1, Application US/10075872
; Patent No. 6500211
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/075,872
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
```



```

; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-10-075-872-1

Query Match      82.5%; Score 33; DB 4; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      60 ADWQWS 65

RESULT 29
US-10-261-997-1
; Sequence 1, Application US/10261997
; Patent No. 6582750
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/261,997
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-10-261-997-1

Query Match      82.5%; Score 33; DB 4; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      60 ADWQWS 65

RESULT 30
US-08-032-848C-9
; Sequence 9, Application US/08032848C
; Patent No. 5475101
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of
; TITLE OF INVENTION: EG III Cellulase
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/032,848C
; FILING DATE: MAR 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.
```

```

; REGISTRATION NUMBER: 33,401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7356
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-032-848C-9

Query Match      82.5%; Score 33; DB 1; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      62 ADWQWS 67

RESULT 31
US-08-438-870-9
; Sequence 9, Application US/08438870
; Patent No. 5753484
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of EG
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,870
; FILING DATE: May 10, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 35,696
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7555
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-438-870-9

Query Match      82.5%; Score 33; DB 1; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      62 ADWQWS 67
```



```
RESULT 32
US-09-146-770-3
; Sequence 3, Application US/09146770
; Patent No. 6187732
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/146,770
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: T. reesei
US-09-146-770-3
Query Match      82.5%; Score 33; DB 3; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||:
Db      62 ADWQWS 67

RESULT 33
US-09-146-770-4
; Sequence 4, Application US/09146770
; Patent No. 6187732
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/146,770
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: H. schweinitzii
US-09-146-770-4
Query Match      82.5%; Score 33; DB 3; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||:
Db      62 ADWQWS 67

RESULT 34
US-09-216-295-3
; Sequence 3, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: T. reesei
US-09-633-084-3
Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||:
Db      62 ADWQWS 67

RESULT 35
US-09-216-295-4
; Sequence 4, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Hypocrea schweinitzii
US-09-216-295-4
Query Match      82.5%; Score 33; DB 3; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||:
Db      62 ADWQWS 67

RESULT 36
US-09-633-084-3
; Sequence 3, Application US/09633084
; Patent No. 6407046
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/633,084
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/146,770
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: T. reesei
US-09-633-084-3
Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||:
Db      62 ADWQWS 67

RESULT 37
US-09-633-084-4
```


[illegible]


```
; Sequence 45, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Gliocladium roseum (1)
US-09-632-575-45

Query Match      82.5%; Score 33; DB 4; Length 238;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      ||||:
Db      66 DWSWS 70

RESULT 48
US-09-216-295-15
; Sequence 15, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328e1 Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Gliocladium roseum (1)
US-09-216-295-15

Query Match      82.5%; Score 33; DB 3; Length 239;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      ||||:
Db      66 DWSWS 70

RESULT 49
US-09-252-991A-17312
; Sequence 17312, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17312
```

```
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17312

Query Match      82.5%; Score 33; DB 4; Length 316;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      ||||:
Db      272 DWAWA 276

RESULT 50
US-08-140-104A-2
; Sequence 2, Application US/08140104A
; Patent No. 5585255
; GENERAL INFORMATION:
; APPLICANT: Tsukada, Yogi
; APPLICANT: Tazuke, Yasuhiko
; APPLICANT: Okada, Shigenori
; APPLICANT: Adachi, Kenichi
; TITLE OF INVENTION: BILE ACID SULFATASE GENE, PLASMID
; TITLE OF INVENTION: CONTAINING SAID GENE AND METHOD OF PRODUCING BILE ACID
; TITLE OF INVENTION: SULFATE SULFATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,104A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP93/00244
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: SAEGU3.001AUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-140-104A-2

Query Match      82.5%; Score 33; DB 1; Length 467;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      ||||:
Db      401 ADWAW 405

Search completed: July 23, 2004, 13:20:23
Job time : 20 secs
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:18:19 ; Search time 42 Seconds
(without alignments)
44.736 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADWSWA 6
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues
Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	10	US-09-847-946A-41
2	40	100.0	6	10	US-09-847-946A-73
3	40	100.0	7	10	US-09-847-946A-77
4	40	100.0	8	10	US-09-847-946A-70
5	40	100.0	8	10	US-09-847-946A-78
6	40	100.0	9	10	US-09-847-946A-69
7	40	100.0	9	10	US-09-847-946A-72
8	40	100.0	9	10	US-09-847-946A-75
9	40	100.0	9	10	US-09-847-946A-76
10	40	100.0	10	10	US-09-847-946A-71
11	40	100.0	10	10	US-09-847-946A-74
12	40	100.0	11	10	US-09-847-946A-68
13	37	92.5	236	12	US-10-441-625-17
14	37	92.5	236	14	US-10-441-626-17
15	37	92.5	885	9	US-09-815-242-5090

16	37	92.5	885	12	US-10-282-122A-43572	Sequence 43572, A
17	36	90.0	6	9	US-09-847-940B-4	Sequence 4, Appli
18	36	90.0	6	9	US-09-847-940B-5	Sequence 5, Appli
19	36	90.0	6	10	US-09-847-946A-4	Sequence 4, Appli
20	36	90.0	6	10	US-09-847-946A-5	Sequence 5, Appli
21	36	90.0	6	10	US-09-847-946A-39	Sequence 39, Appl
22	36	90.0	6	10	US-09-847-946A-40	Sequence 40, Appl
23	36	90.0	6	10	US-09-847-946A-51	Sequence 51, Appl
24	36	90.0	6	10	US-09-847-946A-62	Sequence 62, Appl
25	36	90.0	7	10	US-09-847-946A-55	Sequence 55, Appl
26	36	90.0	7	10	US-09-847-946A-66	Sequence 66, Appl
27	36	90.0	8	10	US-09-847-946A-48	Sequence 48, Appl
28	36	90.0	8	10	US-09-847-946A-56	Sequence 56, Appl
29	36	90.0	8	10	US-09-847-946A-59	Sequence 59, Appl
30	36	90.0	8	10	US-09-847-946A-67	Sequence 67, Appl
31	36	90.0	9	10	US-09-847-946A-47	Sequence 47, Appl
32	36	90.0	9	10	US-09-847-946A-50	Sequence 50, Appl
33	36	90.0	9	10	US-09-847-946A-53	Sequence 53, Appl
34	36	90.0	9	10	US-09-847-946A-54	Sequence 54, Appl
35	36	90.0	9	10	US-09-847-946A-58	Sequence 58, Appl
36	36	90.0	9	10	US-09-847-946A-61	Sequence 61, Appl
37	36	90.0	9	10	US-09-847-946A-64	Sequence 64, Appl
38	36	90.0	9	10	US-09-847-946A-65	Sequence 65, Appl
39	36	90.0	10	10	US-09-847-946A-49	Sequence 49, Appl
40	36	90.0	10	10	US-09-847-946A-52	Sequence 52, Appl
41	36	90.0	10	10	US-09-847-946A-57	Sequence 57, Appl
42	36	90.0	10	10	US-09-847-946A-60	Sequence 60, Appl
43	36	90.0	10	10	US-09-847-946A-63	Sequence 63, Appl
44	36	90.0	11	10	US-09-847-946A-46	Sequence 46, Appl
45	36	90.0	147	12	US-10-424-599-199086	Sequence 199086,
46	36	90.0	173	14	US-10-156-761-15045	Sequence 15045, A
47	36	90.0	174	14	US-10-219-220-163	Sequence 163, App
48	36	90.0	225	14	US-10-219-220-162	Sequence 162, App
49	36	90.0	277	14	US-10-219-220-280	Sequence 280, App
50	36	90.0	312	14	US-10-306-762-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-847-946A-41
; Sequence 41, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

US-09-847-946A-72
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-72
Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
| | | | |
Db 1 ADWSWA 6

RESULT 6
US-09-847-946A-69
; Sequence 69, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-69
Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
| | | | |
Db 1 ADWSWA 6

RESULT 7
US-09-847-946A-72
; Sequence 72, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-72
Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
| | | | |
Db 1 ADWSWA 6

RESULT 8
US-09-847-946A-75
; Sequence 75, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-75
Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
| | | | |
Db 3 ADWSWA 8

RESULT 9
US-09-847-946A-76
; Sequence 76, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-76
Query Match 100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
| | | | |
Db 3 ADWSWA 8

```



```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-76

Query Match      100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
        |||||
Db      2 ADWSWA 7

RESULT 10
US-09-847-946A-71
; Sequence 71, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-71

Query Match      100.0%; Score 40; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
        |||||
Db      2 ADWSWA 7

RESULT 11
US-09-847-946A-74
; Sequence 74, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22

```



```
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-10-441-625-17

Query Match          92.5%; Score 37; DB 12; Length 236;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      63 ADWSWS 68

RESULT 14
US-10-441-626-17
; Sequence 17, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1e1 Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-10-441-626-17

Query Match          92.5%; Score 37; DB 14; Length 236;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      63 ADWSWS 68

RESULT 15
US-09-815-242-5090
; Sequence 5090, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
```

```
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5090
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5090

Query Match          92.5%; Score 37; DB 9; Length 885;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      563 ADMAWA 568

RESULT 16
US-10-282-122A-43572
; Sequence 43572, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43572
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-43572

Query Match          92.5%; Score 37; DB 12; Length 885;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
```


Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWA 6
|||||
Db 563 ADWAWA 568

RESULT 17
US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-4

Query Match 90.0%; Score 36; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 1 ADWSW 5

RESULT 18
US-09-847-940B-5
; Sequence 5, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-5

Query Match 90.0%; Score 36; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 2 DWSWA 6

RESULT 19
US-09-847-946A-4

; Sequence 4, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-4

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 1 ADWSW 5

RESULT 20
US-09-847-946A-5
; Sequence 5, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-5

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 2 DWSWA 6

RESULT 21

US-09-847-946A-39
; Sequence 39, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-39

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 1 ADWSW 5

RESULT 22
US-09-847-946A-40
; Sequence 40, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-40

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 2 DWSWA 6

RESULT 23
US-09-847-946A-51
; Sequence 51, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-51

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 1 ADWSW 5

RESULT 24
US-09-847-946A-62
; Sequence 62, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-62

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
| | | | |
Db 2 DWSWA 6

RESULT 25
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-55

Query Match 90.0%; Score 36; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
| | | | |
Db 1 ADWSW 5

RESULT 26
US-09-847-946A-66
; Sequence 66, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-66

Query Match 90.0%; Score 36; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
| | | | |
Db 2 DWSWA 6

RESULT 27
US-09-847-946A-48
; Sequence 48, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-48

Query Match 90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
| | | | |
Db 3 ADWSW 7

RESULT 28
US-09-847-946A-56
; Sequence 56, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence


```
US-09-847-946A-56
Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      1 ADWSW 5

RESULT 29
US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-59

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      4 DWSWA 8

RESULT 30
US-09-847-946A-67
; Sequence 67, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-67

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      1 ADWSW 5

RESULT 29
US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-59

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      4 DWSWA 8

RESULT 30
US-09-847-946A-67
; Sequence 67, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-67

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      1 ADWSW 5

RESULT 29
US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-59

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      2 DWSWA 6

RESULT 31
US-09-847-946A-47
; Sequence 47, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-47

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      1 ADWSW 5

RESULT 32
US-09-847-946A-50
; Sequence 50, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
```



```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-50

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      1 ADWSW 5

RESULT 33
US-09-847-946A-53
; Sequence 53, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-53

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      3 ADWSW 7

RESULT 34
US-09-847-946A-54
; Sequence 54, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
;

```

```

; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-54

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      2 ADWSW 6

RESULT 35
US-09-847-946A-58
; Sequence 58, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-58

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
Db      2 DWSWA 6

RESULT 36
US-09-847-946A-61
; Sequence 61, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
;

```



```

; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-61

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      2 DWSWA 6

RESULT 37
US-09-847-946A-64
; Sequence 64, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-64

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      4 DWSWA 8

RESULT 38
US-09-847-946A-65
; Sequence 65, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
```

```

; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 160
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-65

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      3 DWSWA 7

RESULT 39
US-09-847-946A-49
; Sequence 49, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-49

Query Match          90.0%; Score 36; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
      |||||
Db      2 ADWSW 6

RESULT 40
US-09-847-946A-52
; Sequence 52, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
```


; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-46

Query Match 90.0%; Score 36; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 3 ADWSW 7

RESULT 45
US-10-424-599-199086
; Sequence 199086, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199086
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2179C.1.pap
US-10-424-599-199086

Query Match 90.0%; Score 36; DB 12; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 75 DWSWA 79

RESULT 46
US-10-156-761-15045
; Sequence 15045, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 15045
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-15045

Query Match 90.0%; Score 36; DB 14; Length 173;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 53 ADWEWA 58

RESULT 47
US-10-219-220-163
; Sequence 163, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-163

Query Match 90.0%; Score 36; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 109 ADWSW 113

RESULT 48
US-10-219-220-162
; Sequence 162, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-162

Query Match 90.0%; Score 36; DB 14; Length 225;
Best Local Similarity 100.0%; Pred.No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 100 ADWSW 104

RESULT 49
US-10-219-220-280
; Sequence 280, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-280

Query Match 90.0%; Score 36; DB 14; Length 277;
Best Local Similarity 100.0%; Pred.No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 95 ADWSW 99

RESULT 50
US-10-306-762-23
; Sequence 23, Application US/10306762
; Publication No. US20030187220A1
; GENERAL INFORMATION:
; APPLICANT: Park, Frances
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
; TITLE OF INVENTION: MONONUCLEOTIDE BINDING PROTEIN (FMNBP)
; FILE REFERENCE: 52498-20011.00
; CURRENT APPLICATION NUMBER: US/10/306,762
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US 60/334,132
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 312
; TYPE: PRT
; ORGANISM: C. hutchinsonii (23137247)
US-10-306-762-23

Query Match 90.0%; Score 36; DB 14; Length 312;
Best Local Similarity 100.0%; Pred.No. 9.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
|||||
Db 171 ADWSW 175
Search completed: July 23, 2004, 13:21:16
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:16:29 ; Search time 16 Seconds
(without alignments)
36.072 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	610	2 T35222	hypothetical prote
2	37	92.5	885	2 C83441	two-component sens
3	36	90.0	374	2 B83241	conserved hypothet
4	36	90.0	889	2 E87304	TonB-dependent rec
5	34	85.0	275	2 T05822	hypothetical prote
6	34	85.0	617	2 C84922	probable protein k
7	34	85.0	1842	2 T43409	probable fatty-aci
8	34	85.0	1842	2 T38781	fatty acid synthas
9	33	82.5	132	2 S65785	mel-13a protein -
10	33	82.5	198	2 B82531	conserved hypothet
11	33	82.5	220	2 D64316	restriction modifi
12	33	82.5	232	2 S58353	CdiB protein - she
13	33	82.5	239	2 D90470	hypothetical prote
14	33	82.5	257	2 D87152	conserved hypothet
15	33	82.5	276	2 B75337	hypothetical prote
16	33	82.5	304	2 F83632	probable cytochrom
17	33	82.5	310	2 JC7853	L-fucose-specific
18	33	82.5	324	2 AB3548	vegetatible incom
19	33	82.5	328	2 E72424	oligopeptide ABC t
20	33	82.5	333	2 S47246	gene Cdi protein -
21	33	82.5	350	2 S71923	cysteine proteinas
22	33	82.5	368	2 H90998	probable proteinas
23	33	82.5	410	2 D75475	lycopen cyclase -
24	33	82.5	415	2 AE1844	hypothetical prote
25	33	82.5	418	2 AE1460	sugar ABC transpor
26	33	82.5	418	2 AF1097	sugar ABC transpor
27	33	82.5	421	2 T38242	probable phosphata
28	33	82.5	433	2 T31511	hypothetical prote
29	33	82.5	467	2 G82697	hypothetical prote

30	33	82.5	478	2 E89790	6-phospho-beta-glu
31	33	82.5	479	2 I39953	6-phospho-beta-glu
32	33	82.5	492	2 S03098	aerolysin precurs
33	33	82.5	529	2 C86958	probable GMP synth
34	33	82.5	539	2 T15256	hypothetical prote
35	33	82.5	578	2 C64452	restriction modifi
36	33	82.5	590	2 S72813	GMP synthase (glut
37	33	82.5	616	2 C69226	type I restriction
38	33	82.5	623	2 E75221	type I restriction
39	33	82.5	765	2 S76795	hypothetical prote
40	33	82.5	836	2 D82177	conserved hypothet
41	33	82.5	1202	2 S71424	nitric-oxide synth
42	33	82.5	1203	1 A47501	nitric-oxide synth
43	33	82.5	1205	1 A38943	nitric-oxide synth
44	33	82.5	1329	2 D87226	conserved hypothet
45	33	82.5	1409	2 S74916	alkaline phosphat
46	33	82.5	1879	2 S74915	extracellular nucl
47	33	82.5	3005	2 T08841	polyprotein - dour
48	32	80.0	100	2 H81042	hypothetical prote
49	32	80.0	107	1 SSUL	stellacyanin - Jap
50	32	80.0	113	2 A75355	hypothetical prote

ALIGNMENTS

RESULT 1

T35222
hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35222
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21572
A;Accession: T35222
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-610 <SEE>
A;Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SCOEDB:SC5C7.15
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5C7.15

Query Match 92.5%; Score 37; DB 2; Length 610;
Best Local Similarity 83.3%; Pred.No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
|||:|
Db 83 ADWAWA 88

RESULT 2

C83441
two-component sensor KdpD PA1636 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83441
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83441
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-885 <STO>
A;Cross-references: GB:AE004591; GB:AE004091; NID:g9947599; PIDN:AAG05025.1; GSPDB:GN001:
C;Experimental source: strain PA01
C;Genetics:
A;Gene: kdpD; PA1636

Query Match 92.5%; Score 37; DB 2; Length 885;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 563 ADWAWA 568

RESULT 3
B83241
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83241
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bro
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <STO>
A;Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 81 DWSWA 85

RESULT 4
E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87304
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-889 <STO>
A;Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 618 ADWSW 622

RESULT 5
T05822
hypothetical protein T5K18.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: T05822
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Bar
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15453
A;Accession: T05822
A;Molecule type: DNA
A;Residues: 1-275 <BEV>
A;Cross-references: EMBL:AL022580
A;Experimental source: cultivar Columbia; BAC clone T5K18
C;Genetics:
A;Map position: 4
A;Introns: 103/3; 141/3; 169/1; 206/3
A;Note: T5K18.170

Query Match 85.0%; Score 34; DB 2; Length 275;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 57 SDWSWS 62

RESULT 6
C84922
probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84922
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84922
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <STO>
A;Cross-references: GB:AE002093; NID:g4249408; PIDN:AAD13705.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g48010
A;Map position: 2

Query Match 85.0%; Score 34; DB 2; Length 617;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 500 ADWAWS 505

RESULT 7
T43409
probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomy
N;Alternate names: fatty acid synthetase alpha subunit
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43409
R;Saitoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hirata, A.; Yan
J. Cell Biol. 134, 949-961, 1996
A;Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase an
A;Reference number: Z22493; MUID:96354912; PMID:8769419
A;Accession: T43409
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1842 <SAI>
A;Cross-references: EMBL:D83412; NID:g1199959; PIDN:BAA11913.1; PID:g1199960
C;Genetics:
A;Note: lsd1+
C;Superfamily: yeast fatty-acid synthase

C;Keywords: acyltransferase; coenzyme A

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
:||||
Db 400 SDNWA 405

RESULT 8
T38781
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T38781
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: 221751
A;Accession: T38781
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1842 <SKE>
A;Cross-references: EMBL:Z98762; PIDN:CAB11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c
A;Experimental source: strain 972h-; cosmid c4A8
C;Genetics:
A;Gene: SPDB:SPAC4A8.11c
A;Map position: 1
C;Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
:||||
Db 400 SDNWA 405

RESULT 9
S65785
mel-13a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S65785
R;Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene
A;Reference number: S65785; MUID:96180310; PMID:8597592
A;Accession: S65785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <TET>
A;Cross-references: EMBL:U35309
C;Genetics:
A;Gene: mel-13
C;Superfamily: mouse mel-13a protein
C;Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
:||||
Db 57 SDWSW 61

RESULT 10
B82531
conserved hypothetical protein XF2666 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C;Accession: B82531
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <SIM>
A;Cross-references: GB:AE004072; GB:AE003849; NID:g9107884; PIDN:AAF85463.1; GSPDB:GN0012
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tshuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2666
C;Superfamily: conserved hypothetical protein MJ1677

Query Match 82.5%; Score 33; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
:||||
Db 135 DWNWA 139

RESULT 11
D64316
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2002
C;Accession: D64316
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64316
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-220 <BUL>
A;Cross-references: GB:U67470; GB:L77117; NID:g2826247; PIDN:AAB98113.1; PID:g1592267; T
C;Genetics:
A;Map position: REV127472-126810

A;Start codon: TTG
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
:||||
Db 33 ADWAW 37

RESULT 12

S58353
CD1b protein - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C;Accession: S58353
R;Ferguson, E.D.; Dutia, B.M.; Hein, W.; Hopkins, J.
submitted to the EMBL Data Library, July 1995
A;Description: The ovine CD1 gene family contains at least four CD1B homologues.
A;Reference number: S58353
A;Accession: S58353
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <FER>
A;Cross-references: EMBL:X90567; NID:g945010; PIDN:CAA62187.1; PID:g945011
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;115-180/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 232;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 156 ADWTW 160

RESULT 13
D90470
hypothetical protein cysH [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: D90470
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90470
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-239 <KUR>
A;Cross-references: GB:AE006641; NID:g13816282; PIDN:AAK43019.1; GSPDB:GN00155
C;Genetics:
A;Gene: cysH
C;Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 172 ADWTW 176

RESULT 14
D87152
conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: D87152
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>

A;Cross-references: GB:AL450380; NID:g13093601; PIDN:CAC30900.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML1945
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100

Query Match 82.5%; Score 33; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
|:|:|:|
Db 11 ATWSWA 16

RESULT 15
B75337
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: B75337
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; T
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mat
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75337
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <WHI>
A;Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF11479.1; PID:g6459711
A;Experimental source: Strain R1
C;Genetics:
A;Gene: DR1923
A;Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 84 ADWAW 88

RESULT 16
F83632
probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83632
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <STO>
A;Cross-references: GB:AE004449; GB:AE004091; NID:g9945928; PIDN:AAG03503.1; GSPDB:GN0015
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0113
C;Superfamily: heme O synthase

Query Match 82.5%; Score 33; DB 2; Length 304;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||:|

Db 260 DWAWA 264

RESULT 17
JC7853

L-fucose-specific lectin - Aspergillus oryzae
C;Species: Aspergillus oryzae
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 31-Mar-2003
C;Accession: JC7853; PC7191
R;Ishida, H.; Moritani, T.; Hata, Y.; Kawato, A.; Suginami, K.; Abe, Y.; Imayasu, S.
Biosci. Biotechnol. Biochem. 66, 1002-1008, 2002
A;Title: Molecular cloning and overexpression of fleA gene encoding a fucose-specific le
A;Reference number: JC7853; MUID:22087106; PMID:12092808
A;Accession: JC7853
A;Molecule type: DNA
A;Residues: 1-310 <ISH>
A;Cross-references: DDBJ:AB072379
A;Experimental source: strain OSI1018
A;Accession: PC7191
A;Molecule type: protein
A;Residues: 132-147;148-177 <IS2>
C;Comment: This protein, with ferrichrysin-affinity, has hemagglutination activity again
C;Genetics:
A;Gene: fleA
A;Introns: 12/1; 71/3; 143/1; 177/2

Query Match 82.5%; Score 33; DB 2; Length 310;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
:|||||
Db 290 SEWSWA 295

RESULT 18
AB3548

vegetatable incompatibility protein het-e-1 [imported] - Brucella melitensis (strain 16M
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3548
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3548
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53549.1; PID:gl7984458; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0307
A;Map position: II

Query Match 82.5%; Score 33; DB 2; Length 324;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
:|||||
Db 209 DWSWS 213

RESULT 19
E72424

oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72424
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <ARN>
A;Cross-references: GB:AE001692; GB:AE000512; NID:g4980535; PIDN:AAD35154.1; PID:g4980546
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0060
C;Superfamily: oligopeptide permease protein oppB

Query Match 82.5%; Score 33; DB 2; Length 328;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
:|||||
Db 181 APWSWA 186

RESULT 20
S47246

gene CD1 protein - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47246
R;Ferguson, E.E.
submitted to the EMBL Data Library, August 1994
A;Description: Isolation and analysis of cDNA's encoding the ovine homologues of CD1.
A;Reference number: S47246
A;Accession: S47246
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-333 <FER>
A;Cross-references: EMBL:Z36892
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:216-281/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 333;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
:|||||
Db 257 ADWTW 261

RESULT 21
S71923

cysteine proteinase (EC 3.4.22.-) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C;Accession: S71923
R;Jones, C.G.; Tucker, G.A.; Lycett, G.W.
Biochim. Biophys. Acta 1296, 13-15, 1996
A;Title: Pattern of expression and characteristics of a cysteine proteinase cDNA from ge
A;Reference number: S71923; MUID:96350414; PMID:8765223
A;Accession: S71923
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-350 <JON>
A;Cross-references: EMBL:Z68291; NID:gl134881; PIDN:CAA92583.1; PID:gl134882
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F:157,297,317/Active site: Cys, His, Asn #status predicted

Query Match 82.5%; Score 33; DB 2; Length 350;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A;Cross-references: GB:NC_003210; PIDN:CAC98396.1; PID:g16409538; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0181

Query Match 82.5%; Score 33; DB 2; Length 418;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||:|
Db 167 ADWTW 171

RESULT 27
T38242
probable phosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38242
R;Brown, D.; Churcher, C.M.; Bartell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z21781
A;Accession: T38242
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-421 <BRO>
A;Cross-references: EMBL:Z98559; PIDN:CAB11157.1; GSPDB:GN00066; SPDB:SPAC23C11.04c
A;Experimental source: strain 972h-; cosmid c23C11
C;Genetics:
A;Gene: SPDB:SPAC23C11.04c
A;Map position: 1
A;Introns: 181/1; 373/3

Query Match 82.5%; Score 33; DB 2; Length 421;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||:|
Db 93 ADWTW 97

RESULT 28
T31511
hypothetical protein Y116A8C.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T31511
R;McMurray, A.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21041
A;Accession: T31511
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-433 <WIL>
A;Cross-references: EMBL:AL117204; PIDN:CAB55145.1; CESP:Y116A8C.9
A;Experimental source: clone Y116A8C
C;Genetics:
A;Gene: CESP:Y116A8C.9
A;Introns: 16/2; 42/2; 75/2; 107/3; 173/3; 230/3; 262/3; 318/3; 373/1; 398/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.9

Query Match 82.5%; Score 33; DB 2; Length 433;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
|||:|
Db 175 DWTWA 179

RESULT 29

G82697
hypothetical protein XF1318 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82697
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing, Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82697
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-467 <SIM>
A;Cross-references: GB:AE003964; GB:AE003849; NID:g9106300; PIDN:AAF84127.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1318

Query Match 82.5%; Score 33; DB 2; Length 467;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||:|
Db 9 ADWAW 13

RESULT 30
E89790
6-phospho-beta-glucosidase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: E89790
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-478 <KUR>
A;Cross-references: GB:BA000018; PID:g13700182; PIDN:BA01480.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: bglA
C;Superfamily: Agrobacterium beta-glucosidase

Query Match 82.5%; Score 33; DB 2; Length 478;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
:|||
Db 347 SDWGW 352

RESULT 31
I39953
6-phospho-beta-glucosidase (EC 3.2.1.86) bgIA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C;Accession: I39953; F69593
R;Zhang, J.; Aronson, A.I.
Gene 140, 85-90, 1994
A;Title: A Bacillus subtilis bgIA gene encoding phospho-beta-glucosidase is inducible an
A;Reference number: I39953; MUID:94171085; PMID:8125345
A;Accession: I39953
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-479 <RES>
A;Cross-references: GB:L19710; NID:g506380; PIDN:AAA22660.1; PID:g506381
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69593
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-479 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16048.1; PID:g2636558
A;Experimental source: strain 168
C;Genetics:
A;Gene: bgIA
C;Superfamily: Agrobacterium beta-glucosidase
C;Keywords: glycosidase; hydrolase

Query Match 82.5%; Score 33; DB 2; Length 479;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
: : :
Db 347 SDWGWA 352

RESULT 32
S03098
aerolysin precursor - Aeromonas sobria
C;Species: Aeromonas sobria
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 10-Dec-1999
C;Accession: S03098
R;Husslein, V.; Huhle, B.; Jarchau, T.; Lurz, R.; Goebel, W.; Chakraborty, T.
Mol. Microbiol. 2, 507-517, 1988
A;Title: Nucleotide sequence and transcriptional analysis of the aerCaerA region of Aero
A;Reference number: S03097; MUID:89013892; PMID:2459581
A;Accession: S03098
A;Molecule type: DNA
A;Residues: 1-492 <HUS>
A;Cross-references: EMBL:Y00559; NID:g39016; PIDN:CAA68642.1; PID:g39018
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Genetics:
A;Gene: aerA
C;Superfamily: aerolysin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-492/Product: aerolysin #status predicted <MAT>

Query Match 82.5%; Score 33; DB 2; Length 492;

Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
: : :
Db 395 DWNWA 399

RESULT 33
C86958
probable GMP synthase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: C86958
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C86958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <STO>
A;Cross-references: GB:AL450380; NID:gl3092668; PIDN:CAC29903.1; GSPDB:GN00147
C;Genetics:
A;Gene: guaA
C;Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

Query Match 82.5%; Score 33; DB 2; Length 529;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
: : :
Db 487 ADWTW 491

RESULT 34
T15256
hypothetical protein K07B1.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15256
R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid K07B1.
A;Reference number: Z18317
A;Accession: T15256
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-539 <PAU>
A;Cross-references: EMBL:AF003384; NID:g2088817; PID:g2088823; PIDN:AAB54241.1; GSPDB:GN
A;Experimental source: strain Bristol N2; clone K07B1
C;Genetics:
A;Gene: CESP:K07B1.7
A;Map position: 5
A;Introns: 34/1; 79/3; 313/1; 355/2; 406/2; 466/2; 500/2

Query Match 82.5%; Score 33; DB 2; Length 539;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
: : :
Db 317 DWAWA 321

RESULT 35
C64452
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: C64452
R;Bult, C.J.; White, O.; Oleen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: C64452
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-578 <BUL>
A;Cross-references: GB:U67563; GB:L77117; NID:g2826379; PIDN:AAB99225.1; PID:g1592326; T
C;Genetics:
A;Map position: REV1163994-1162258
A;Start codon: TTG
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 82.5%; Score 33; DB 2; Length 578;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 391 ADWAW 395

RESULT 36
S72813
GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) - Mycobacterium leprae
N;Alternate names: GMP synthetase guaA; protein B1620_C2_205
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72813
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1620.
A;Reference number: S72584
A;Accession: S72813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <SMI>
A;Cross-references: EMBL:U00015; NID:g466931; PIDN:AAC43222.1; PID:g466934
C;Genetics:
A;Gene: guaA
C;Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology
C;Keywords: ligase; purine nucleotide biosynthesis
F;78-257/Domain: trpG homology <TRG>
F;298-465/Domain: GMP binding #status predicted <GMP>
F;154/Active site: Cys #status predicted

Query Match 82.5%; Score 33; DB 2; Length 590;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 548 ADWTW 552

RESULT 37
C69226
type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: C69226
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: C69226
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-616 <MTH>
A;Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AAB85440.1; PID:g262204
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH942
A;Start codon: GTG
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 82.5%; Score 33; DB 2; Length 616;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 425 ADWAW 429

RESULT 38
E75221
type I restriction modification enzyme, chain m. PAB2149 - Pyrococcus abyssi (strain Orsa
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: E75221
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A;Reference number: A75001
A;Accession: E75221
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-623 <KAW>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49220.1; PID:g545772
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2149
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 82.5%; Score 33; DB 2; Length 623;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 434 ADWAW 438

RESULT 39
S76795
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76795
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76795
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-765 <KAN>
A;Cross-references: EMBL:D90916; GB:AB001339; NID:gl653715; PIDN:BAA18707.1; PID:dl01944
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 82.5%; Score 33; DB 2; Length 765;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ADWSW 5		
Db	708	ADWNW 712		
RESULT 40				
D82177				
conserved hypothetical protein VC1629 [imported] - Vibrio cholerae (strain N16961 serogroup O1; serotype El Tor)				
C;Species: Vibrio cholerae				
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001				
C;Accession: D82177				
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.				
Nature 406, 477-483, 2000				
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.				
A;Reference number: A82035; MUID:20406833; PMID:10952301				
A;Accession: D82177				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-836 <HEI>				
A;Cross-references: GB:AE004240; GB:AE003852; NID:g9656133; PIDN:AAF94780.1; GSPDB:GN001				
A;Experimental source: serogroup O1; strain N16961; biotype El Tor				
C;Genetics:				
A;Gene: VC1629				
A;Map position: 1				
Query Match 82.5%; Score 33; DB 2; Length 836;				
Best Local Similarity 80.0%; Pred. No. 6.1e+02;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
Qy	2	DWSWA 6		
Db	356	DWSWS 360		
RESULT 41				
S71424				
nitric-oxide synthase (EC 1.14.13.39), endothelial - mouse				
C;Species: Mus musculus (house mouse)				
C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 04-Mar-2000				
C;Accession: S71424				
R;Gnanapandithen, K.; Chen, Z.; Kau, C.L.; Gorczynski, R.M.; Marsden, P.A.				
Biochim. Biophys. Acta 1308, 103-106, 1996				
A;Title: Cloning and characterization of murine endothelial constitutive nitric oxide synthase				
A;Reference number: S71424; MUID:96350460; PMID:8764825				
A;Accession: S71424				
A;Molecule type: mRNA				
A;Residues: 1-1202 <GNA>				
A;Cross-references: EMBL:U53142; NID:G1518955; PIDN:AAC52766.1; PID:G1518956				
A;Experimental source: fetal cardiac				
C;Genetics:				
A;Gene: NOS				
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reductase				
C;Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN				
F;490-509/Region: calmodulin binding #status predicted				
F;519-1158/Domain: NADPH-ferrihemoprotein reductase homology <FEH>				
F;521-702/Domain: flavodoxin homology <FLX>				
F;647-679/Region: FMN binding #status predicted				
F;790-803/Region: FAD-pyrophosphate binding #status predicted				
F;934-945/Region: FAD-isoalloxazine binding #status predicted				
F;1009-1027/Region: NADP-ribose binding #status predicted				
F;1107-1123/Region: NADP-adenine binding #status predicted				
F;12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted				
F;3/Modified site: aspartic acid (Asn) #status predicted				
F;183/Binding site: heme iron (Cys) (axial ligand) #status predicted				
Query Match 82.5%; Score 33; DB 2; Length 1202;				
Best Local Similarity 80.0%; Pred. No. 8.8e+02;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	ADWSW 5		

A;Gene: GDB:NOS3
A;Cross-references: GDB:209976; OMIM:163729
A;Map position: 7q36-7q36
A;Introns: 53/2; 90/3; 140/2; 194/3; 225/2; 272/3; 319/2; 377/3; 411/3; 476/3; 501/2; 54
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN
F;491-509/Region: calmodulin binding #status predicted
F;520-1159/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;522-703/Domain: flavodoxin homology <FLX>
F;648-680/Region: FMN binding #status predicted
F;791-804/Region: FAD-pyrophosphate binding #status predicted
F;935-946/Region: FAD-isalloxazine binding #status predicted
F;1010-1028/Region: NADP-ribose binding #status predicted
F;1108-1124/Region: NADP-adenine binding #status predicted
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Modified site: aspartic acid (Asn) #status predicted
F;184/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 82.5%; Score 33; DB 1; Length 1203;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 443 ADWAW 447

RESULT 43
A38943
nitric-oxide synthase (EC 1.14.13.39), endothelial - bovine
N;Alternate names: ECNOS; nitric-oxide synthase type III
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Jun-1995 #sequence revision 02-Jun-1995 #text_change 03-Mar-2000
C;Accession: A38943; A46033; I45945; A42841; I45946; A38944
R;Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.
submitted to GenBank, July 1992
A;Reference number: A38943
A;Accession: A38943
A;Molecule type: mRNA
A;Residues: 1-1205 <LAM1>
A;Cross-references: GB:M89952; NID:g162976; PIDN:AAA30494.1; PID:g162977
A;Experimental source: aortic endothelial cells
R;Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 6348-6352, 1992
A;Title: Endothelial nitric oxide synthase: molecular cloning and characterization of a
A;Reference number: A46033; MUID:92335295; PMID:1378626
A;Accession: A46033
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-860, 'I', 862-1205 <LAM2>
A;Cross-references: GB:M89952; NID:g162976
A;Experimental source: endothelial
A;Note: sequence extracted from NCBI backbone (NCBIP:108720)
R;Nishida, K.; Harrison, D.G.; Navas, J.P.; Fisher, A.A.; Dockery, S.P.; Nerem, R.M.; AL
J. Clin. Invest. 90, 2092-2096, 1992
A;Title: Molecular Cloning and Characterization of the constitutive bovine aortic Endoth
A;Reference number: I45945; MUID:93055452; PMID:1385480
A;Accession: I45945
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1205 <NIS>
A;Cross-references: GB:M99057; NID:g163421; PIDN:AAA30667.1; PID:g163422
R;Sessa, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly
J. Biol. Chem. 267, 15274-15276, 1992
A;Title: Molecular cloning and expression of a cDNA encoding endothelial cell nitric oxi
A;Reference number: A42841; MUID:92348367; PMID:1379225
A;Accession: A42841
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-51, 'N', 53-99, 'R', 101-147, 'M', 149-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-3
A;Cross-references: GB:M95674; NID:g163426; PIDN:AAA30669.1; PID:g163427
A;Experimental source: aortic endothelial cells
A;Note: submitted to GenBank, August 1992
A;Note: GenBank entry BOVNOS, release 103.0, has a typographical error in the reference c
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN;
F;493-512/Region: calmodulin binding #status predicted
F;522-1161/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;524-705/Domain: flavodoxin homology <FLX>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Modified site: aspartic acid (Asn) #status predicted
F;186/Binding site: heme iron (Cys) (axial ligand) #status predicted

A;Experimental source: aortic endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typogr
A;Accession: I45946
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99, 'R', 101-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-454, 'Y', 456-458, 'P', 460-
A;Cross-references: GB:M95674; NID:g163426; PIDN:AAA30669.1; PID:g163427
A;Experimental source: aortic endothelial cells
A;Note: submitted to GenBank, August 1992
A;Note: GenBank entry BOVNOS, release 103.0, has a typographical error in the reference c
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN;
F;493-512/Region: calmodulin binding #status predicted
F;522-1161/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;524-705/Domain: flavodoxin homology <FLX>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Modified site: aspartic acid (Asn) #status predicted
F;186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 82.5%; Score 33; DB 1; Length 1205;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 445 ADWAW 449

RESULT 44
D87226
conserved hypothetical protein ML2535 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87226
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87226
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1329 <STO>
A;Cross-references: GB:AL450380; NID:g13093796; PIDN:CAC32066.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML2535

Query Match 82.5%; Score 33; DB 2; Length 1329;
Best Local Similarity 80.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
:||||
Db 260 SDWSW 264

RESULT 45
S74916
alkaline phosphatase - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sl10654
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74916
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.

A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1409 <KAN>
A;Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAA16956.1; PID:d101768
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 82.5%; Score 33; DB 2; Length 1409;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 1370 ADWNW 1374

RESULT 46
S74915
extracellular nuclease - Synchocystis sp. (strain PCC 6803)
N;Alternate names: protein sll0656
C;Species: Synchocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74915
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74915
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1879 <KAN>
A;Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAA16955.1; PID:d101768
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: nuch
A;Start codon: GTG

Query Match 82.5%; Score 33; DB 2; Length 1879;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 1847 ADWNW 1851

RESULT 47
T08841
polyprotein - douroucouli hepatitis GB virus A
C;Species: douroucouli hepatitis GB virus A
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T08841
R;Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.; Mushahwar, I.K.
J. Gen. Virol. 79, 41-45, 1998
A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.
A;Reference number: Z16486; MUID:98120818; PMID:9460920
A;Accession: T08841
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3005 <ERK>
A;Cross-references: EMBL:AF023425; NID:g2828599; PIDN:AAC40502.1; PID:g2828600
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein

Query Match 82.5%; Score 33; DB 2; Length 3005;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 759 SDWSW 763
:||||
RESULT 48
H81042
hypothetical protein NMB1782 [imported] - Neisseria meningitidis (strain MC58 serogroup I
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: H81042; G81988
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <TET>
A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42122.1; PID:g722703;
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:2022556; PMID:10761919
A;Accession: G81988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83970.1; PID:g737941
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB1782; NMA0683; NMA0684
C;Superfamily: Neisseria meningitidis hypothetical protein NMB1782

Query Match 80.0%; Score 32; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
||||
Db 77 DWSW 80

RESULT 49
SSUL
stellacyanin - Japanese lacquer-tree
C;Species: Rhus vernicifera (Japanese lacquer-tree)
C;Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 04-Nov-2002
C;Accession: A00311
R;Bergman, C.; Gandvik, E.K.; Nyman, P.O.; Strid, L.
Biochem. Biophys. Res. Commun. 77, 1052-1059, 1977
A;Title: The amino acid sequence of stellacyanin from the lacquer tree.
A;Reference number: A90206; MUID:77266668; PMID:901509
A;Accession: A00311
A;Molecule type: protein
A;Residues: 1-107 <BER>
R;Bergman, C.; Gandvik, E.K.; Nyman, P.O.; Strid, L.
Biochem. Biophys. Res. Commun. 79, 1013, 1977
A;Reference number: A90207
A;Contents: annotation; erratum
R;Engeseth, H.R.; Hermodson, M.A.; McMillin, D.R.
FEBS Lett. 171, 257-261, 1984
A;Title: A new assignment of the disulfide linkage in stellacyanin.
A;Reference number: A91324; MUID:84208877; PMID:6723985
A;Contents: annotation; disulfide bond
C;Comment: This is a blue, type 1 copper glycoprotein.
C;Superfamily: stellacyanin
C;Keywords: copper; electron transfer; glycoprotein
F;28,60,102/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;46,87,92,97/Binding site: copper (His, Cys, His, Gln) #status predicted
F;59-93/Disulfide bonds: #status experimental

Query Match 80.0%; Score 32; DB 1; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWSWA 6
|||
Db 22 DWKWA 26

RESULT 50
A75355
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: A75355
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <WHI>
A;Cross-references: GB:AE002019; GB:AE000513; NID:g6459547; PIDN:AAF11336.1; PID:g645955
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1779
A;Map position: 1

Query Match 80.0%; Score 32; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWSWA 6
|||
Db 28 DWKWA 32

Search completed: July 23, 2004, 13:19:54
Job time : 17 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:14:03 ; Search time 14 Seconds
(without alignments)
22.316 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	36	90.0	470	1	NRAM_IADBU Q07570 influenza a
2	36	90.0	470	1	NRAM_IADCH Q07571 influenza a
3	36	90.0	470	1	NRAM_IADH2 Q07572 influenza a
4	36	90.0	470	1	NRAM_IADM2 Q07573 influenza a
5	36	90.0	470	1	NRAM_IADU3 Q07599 influenza a
6	36	90.0	470	1	NRAM_IAGEN Q07574 influenza a
7	36	90.0	470	1	NRAM_IAHGD Q07577 influenza a
8	36	90.0	470	1	NRAM_IAHJI Q07578 influenza a
9	36	90.0	470	1	NRAM_IAMAE Q07583 influenza a
10	36	90.0	470	1	NRAM_IATKL Q07585 influenza a
11	36	90.0	598	1	MRJ5_APIME Q97432 apis mellif
12	34	85.0	376	1	PGLR_PENGR Q93883 penicillium
13	34	85.0	1842	1	FAS2_SCHPO Q10289 s fatty aci
14	33	82.5	99	1	NOS3_SHEEP P79209 ovis aries
15	33	82.5	220	1	Y132_METJA Q57596 methanococc
16	33	82.5	232	1	C1B3_SHEEP P80943 ovis aries
17	33	82.5	333	1	C1B2_SHEEP Q29422 ovis aries
18	33	82.5	410	1	Y801_DEIRA Q9rw68 deinococcus
19	33	82.5	421	1	PNK1_SCHPO O13911 schizosacch
20	33	82.5	470	1	NRAM_IAQIT Q07584 influenza a
21	33	82.5	479	1	BGLA_BACSU P42973 bacillus su
22	33	82.5	492	1	AERA_AERTR P09166 aeromonas t
23	33	82.5	529	1	GUAA_MYCLE P46810 mycobacteri
24	33	82.5	578	1	YC20_METJA Q58617 methanococc
25	33	82.5	579	1	YC12_KLEPN Q84458 klebsiella
26	33	82.5	817	1	PHK_STRCO Q8ck51 streptomyc
27	33	82.5	914	1	GUX2_CLOSR P50900 clostridium
28	33	82.5	1201	1	NOS3_MOUSE P70313 mus musculu
29	33	82.5	1202	1	NOS3_HUMAN P29474 homo sapien
30	33	82.5	1204	1	NOS3_BOVIN P29473 bos taurus
31	33	82.5	1204	1	NOS3_PIG Q28969 sus scrofa
32	32	80.0	100	1	NOS3_CAVPO P97270 cavia porce
33	32	80.0	107	1	STEL_RHUV P00302 rhus vernic

RESULT 1
NRAM_IADBU
ID_NRAM_IADBU STANDARD; PRT; 470 AA.
AC Q07570;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.

ALIGNMENTS

OS Influenza A virus (strain A/Duck/Burjatia/652/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoaka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

CC EMBL; L06572; AAA43365.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.

FT ACT SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51989 MW; D1A6F07460F6F8AD CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 2
NRAM_IADCH STANDARD; PRT; 470 AA.
AC Q07571;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; L06573; AAA43367.1; --.
HSSP; P06820; 2BAT.
InterPro; IPR001860; Glyco_hydro_34.
Pfam; PF00064; neur; 1.
ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 169AB89FBE8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 3
NRAM_IADH2. STANDARD; PRT; 470 AA.
AC Q07572;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; L06574; AAA43372.1; --.
HSSP; P06820; 2BAT.
InterPro; IPR001860; Glyco_hydro_34.
Pfam; PF00064; neur; 1.
ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52015 MW; E1C1D3E2C650B93C CRC64;

Query Match		90.0%;	Score 36;	DB 1;	Length 470;							
Best Local Similarity		100.0%;	Pred. No. 70;									
Matches		5;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;							
QY	1 ADWSW 5											
Db	453 ADWSW 457											
RESULT 4												
NRAM_IADM2	STANDARD;	PRT;	470 AA.									
ID_NRAM_IADM2	Q07573;											
AC	01-FEB-1995 (Rel. 31, Created)											
DT	01-FEB-1995 (Rel. 31, Last sequence update)											
DT	28-FEB-2003 (Rel. 41, Last annotation update)											
DE	Neuraminidase (EC 3.2.1.18).											
GN	NA.											
OS	Influenza A virus (strain A/Duck/Memphis/928/74).											
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;											
OC	Influenza A viruses; Influenzavirus A.											
OX	NCBI_TaxID=11367;											
RN	[1]											
RP	SEQUENCE FROM N.A.											
RX	MEDLINE=93212520; PubMed=8460490;											
RA	Saito T., Kawaoka Y., Webster R.G.;											
RT	"Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses.";											
RL	Virology 193:868-876(1993).											
CC	-1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.											
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.											
CC	-1- SUBUNIT: Homotetramer.											
CC	-1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.											
CC	-1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.											
CC	-----											
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).											
CC	-----											
DR	EMBL; L06575; AAA43404.1; -.											
DR	HSSP; P06820; 2BAT.											
DR	InterPro; IPR001860; Glyco_hydro_34.											
DR	Pfam; PF00064; neur; 1.											
DR	ProDom; PD000431; Glyco_hydro_34; 1.											
KW	Hydrolase; Glycosidase; Glycoprotein; Transmembrane.											
FT	TRANSMEM 7 38											
FT	DOMAIN 39 88											
FT	DOMAIN 89 470											
FT	ACT_SITE 273 273											
FT	ACT_SITE 275 275											
FT	CARBOHYD 46 46											
FT	CARBOHYD 54 54											
FT	CARBOHYD 84 84											
FT	CARBOHYD 144 144											
FT	CARBOHYD 293 293											
FT	CARBOHYD 398 398											
SQ	SEQUENCE 470 AA; 52146 MW; 30F5F9FE364C1F49 CRC64;											
Query Match												
Best Local Similarity		90.0%;	Score 36;	DB 1;	Length 470;							
Matches		5;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;							

QY	1 ADWSW 5				
Db	453 ADWSW 457				
RESULT 5					
NRAM_IADU3	STANDARD;	PRT;	470 AA.		
ID	Q07599;				
AC	01-OCT-1994 (Rel. 30, Created)				
DT	01-OCT-1994 (Rel. 30, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Neuraminidase (EC 3.2.1.18).				
GN	NA.				
OS	Influenza A virus (strain A/Duck/Ukraine/1/63).				
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;				
OC	Influenza A viruses; Influenzavirus A.				
OX	NCBI_TaxID=11374;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93212520; PubMed=8460490;				
RA	Saito T., Kawaoka Y., Webster R.G.;				
RT	"Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses.";				
RL	Virology 193:868-876(1993).				
CC	-1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.				
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.				
CC	-1- SUBUNIT: Homotetramer.				
CC	-1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.				
CC	-1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; L06576; AAA16234.1; -.				
DR	HSSP; P06820; 2BAT.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	Pfam; PF00064; neur; 1.				
DR	ProDom; PD000431; Glyco_hydro_34; 1.				
KW	Hydrolase; Glycosidase; Glycoprotein; Transmembrane.				
FT	TRANSMEM 7 37	ANCHOR (BY SIMILARITY).			
FT	DOMAIN 38 88	HYPERVARIABLE STALK REGION.			
FT	DOMAIN 89 470	HEAD OF NEURAMINIDASE.			
FT	ACT_SITE 273 273	PROBABLE.			
FT	ACT_SITE 275 275	PROBABLE.			
FT	CARBOHYD 46 46	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 54 54	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 84 84	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 144 144	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 398 398	N-LINKED (GLCNAC. . .) (POTENTIAL).			
SQ	SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;				
Query Match 90.0%; Score 36; DB 1; Length 470;					
Best Local Similarity 100.0%; Pred. No. 70;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 ADWSW 5				
Db	453 ADWSW 457				

QY	1 ADWSW 5
Db	453 ADWSW 457

GN NA.
OS Influenza A virus (strain A/Equine/Jillln/1/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
DR EMBL; L06579; AAA43374.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 9
NRAM_IAMAE
ID_NRAM_IAMAE STANDARD; PRT; 470 AA.
AC Q07583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.

OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
DR EMBL; L06586; AAA43369.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E11F2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 10
NRAM_IATKL
ID_NRAM_IATKL STANDARD; PRT; 470 AA.
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;

RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; LO6588; AAA43410.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD00431; Glyco_hydro_34; 1.
CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM 7 38
CC DOMAIN 39 88 ANCHOR (BY SIMILARITY).
CC DOMAIN 89 470 HYPERVARIABLE STALK REGION.
CC ACT_SITE 273 273 HEAD OF NEURAMINIDASE.
CC ACT_SITE 275 275 BY SIMILARITY.
CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 470 AA; 52352 MW; DE573742ABFF1E6B CRC64;
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 453 ADWSW 457
RESULT 11
MRJ5 APIME STANDARD; PRT; 598 AA.
ID MRJ5 APIME
AC O97432;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=99373663; PubMed=10441680;
RA Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.;
RT "The family of major royal jelly proteins and its evolution.";

J. Mol. Evol. 49:290-297(1999).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
CC HONEYBEE QUEEN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
CC -!- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
CC the nurse honey bee.
CC -!- SIMILARITY: Belongs to the major royal jelly protein family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF004842; AAD01205.1; -.
CC InterPro; IPR003534; Royaljelly.
CC Pfam; PF03022; MRJP; 2.
CC PRINTS; PR01366; ROYALJELLY.
CC SIGNAL; Repeat; Glycoprotein.
CC CHAIN 1 17 POTENTIAL.
CC FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
CC FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 598 AA; 70236 MW; 2C603C77E7ACDF63 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSWA 6
Db 113 DWSWA 117
RESULT 12
PGLR PENG R STANDARD; PRT; 376 AA.
ID PGLR PENG R
AC O93883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
GN PGG1.
OS Penicillium griseoroseum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=84562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCT 6421;
RA Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;
RT "Cloning and characterization of a gene encoding the
RT endopolygalacturonase of Penicillium griseoroseum.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -!- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).


```

CC -----
DR EMBL; AF085238; AAC83692.1; -
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006626; PbH1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; PbH1_5.
DR PROSITE; PS00502; POLYGALACTURONASE; 1.
KW Hydrolase; Glycosidase; Cell wall; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 376 POLYGALACTURONASE.
SQ SEQUENCE 376 AA; 38068 MW; 1EDB1EC56ED56928 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 376;
Best Local Similarity 66.7%; Pred. No. 1.le+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
   :|||:
DB 349 SDWSWS 354

RESULT 13
FAS2 SCHPO STANDARD; PRT; 1842 AA.
AC Q10289; O14163; P78973;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fatty acid synthase subunit alpha (EC 2.3.1.86) [Includes:
DE Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase
DE (EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier
DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].
DE FAS2 OR LSD1 OR SPAC4A8.11C.
GN Schizosaccharomyces pombe (Fission yeast).
OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96354912; PubMed=8769419;
RA Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,
RA Hirata A., Yanagida M.;
RA "Aberrant mitosis in fission yeast mutants defective in fatty acid
RA synthetase and acetyl CoA carboxylase.";
RA J. Cell Biol. 134:949-961(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M.;
RA "Very long-chain fatty-acid-containing phospholipids accumulate in
RA fatty acid synthase temperature-sensitive mutant strains of the
RA fission yeast Schizosaccharomyces pombe fas2/lcd1.";
RA Biochim. Biophys. Acta 1532:223-233(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

```



```
FT DOMAIN ? 1842 BETA-KETOACYL SYNTHASE.
FT BINDING 180 180 PHOSPHOPANTETHEINE (BY SIMILARITY).
FT ACT SITE 1262 1262 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT CONFLICT 107 107 S -> A (IN REF. 4).
FT CONFLICT 422 422 K -> R (IN REF. 1).
SQ SEQUENCE 1842 AA; 202168 MW; E4019F2D133EE571 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 400 SDWNWA 405

RESULT 14
NOS3_SHEEP
ID_NOS3_SHEEP STANDARD; PRT; 99 AA.
AC P79209;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).
DE NOS3 OR ENOS.
GN Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RA Aguan K., Weiner C.P.;
RT "Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase.";
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RL
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. No mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets (By similarity).
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the NOS family.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; U76738; AAB40705.1; -.
DR HSSP; P29473; 1DOC.
DR InterPro; IPR004030; NO_synthase.
DR Pfam; PF02898; NO synthase; 1.
DR PROSITE; PS60001; NOS; PARTIAL.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
KW Heme; Multigene family.
FT NON_TER 1 1
FT NON_TER 99 99
```

```
SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;

Query Match 82.5%; Score 33; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 65 ADWAW 69

RESULT 15
Y132_METJA
ID_Y132_METJA STANDARD; PRT; 220 AA.
AC Q57596;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0132.
GN MJ0132.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
RL Science 273:1058-1073 (1996).
CC -!- SIMILARITY: TO M.JANNASCHII MJ1220 AND MJEC142.
CC -!- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES (M SUBUNIT).
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; U67470; AAB98113.1; -.
DR PIR; D64316; D64316.
DR TIGR; MJ0132; -.
DR InterPro; IPR003356; N6_DNA_Mtase.
DR Pfam; PF02384; N6_Mtase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 220 AA; 25766 MW; 710DDAB4C7A47954 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 220;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 33 ADWAW 37

RESULT 16
C1B3_SHEEP
ID_C1B3_SHEEP STANDARD; PRT; 232 AA.
AC P80943;
DT 16-OCT-2001 (Rel. 40, Created)
```


DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD1b-3 (CD1b-3 antigen) (SCD1T10)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal thymocytes;
RX MEDLINE=96269982; PubMed=8662069;
RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
RT "The sheep CD1 gene family contains at least four CD1B homologues.";
RL Immunogenetics 44:86-96(1996).
CC -!- FUNCTION: Not known.
CC -!- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By
similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; X90567; CAA62187.1; -.
DR PIR; S58353; S58353.
DR HSSP; P11609; 1CD1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Transmembrane; Multigene family.
FT NON_TER 1 1
FT DOMAIN <1 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222 POTENTIAL.
FT DOMAIN 223 232 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 84 194 IG-LIKE.
FT DISULFID 19 83 BY SIMILARITY.
FT DISULFID 123 178 BY SIMILARITY.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 232 AA; 26023 MW; C96DB93840B56158 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 232;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 156 ADWTW 160
RESULT 17
C1B2_SHEEP STANDARD; PRT; 333 AA.
AC Q29422;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD1b-2 precursor (CD1b-2 antigen)
DE (SCD1B-42) (Antigen IAH-CC14).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=96269982; PubMed=8662069;
RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
RT "The sheep CD1 gene family contains at least four CD1B homologues.";
RL Immunogenetics 44:86-96(1996).
RN [2]
RP SEQUENCE OF 21-33.
RX MEDLINE=99115506; PubMed=9914336;
RA Rhind S.M., Hopkins J., Dutia B.M.;
RT "Amino-terminal sequencing of sheep CD1 antigens and identification of
a sheep CD1D gene.";
RL Immunogenetics 49:225-230(1999).
CC -!- FUNCTION: Not known.
CC -!- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By
similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; Z36891; CAA85360.1; -.
DR PIR; S47246; S47246.
DR HSSP; P11609; 1CD1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Glycoprotein; Signal; Immunoglobulin domain; Transmembrane;
KW Multigene family.
FT SIGNAL 1 20
FT CHAIN 21 333 T-CELL SURFACE GLYCOPROTEIN CD1B-2.
FT DOMAIN 21 302 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 303 323 POTENTIAL.
FT DOMAIN 324 333 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 185 295 IG-LIKE.
FT DISULFID 120 184 BY SIMILARITY.
FT DISULFID 224 279 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 333 AA; 37039 MW; 861BAE9617DB9BA1 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 333;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 257 ADWTW 261
RESULT 18
Y801_DEIRA STANDARD; PRT; 410 AA.
ID Y801 DEIRA
AC Q9RW68;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative carotenoid cyclase DR0801.
GN DR0801.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]

SEQUENCE FROM N.A.
STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
"Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
Science 286:1571-1577(1999).
-!- SIMILARITY: Belongs to the lycopene cyclase family.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; AE001934; AAF10377.1; -.
PIR; D75475; D75475.
TIGR; DR0801; -.
InterPro; IPR008671; Lycopene_cycl.
InterPro; IPR003042; Rng_mnoxygenase.
Pfam; PF05834; Lycopene_cycl; 1.
PRINTS; PR00420; RNMGNXGNASE.
Hypothetical protein; Oxidoreductase; NAD; Carotenoid biosynthesis;
Complete proteome.
NP BIND 11 39 NAD (POTENTIAL).
SEQUENCE 410 AA; 43161 MW; E1B3162F10F9EGAF CRC64;

Query Match 82.5%; Score 33; DB 1; Length 410;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 102 ADWTW 106

RESULT 19
PNK1 SCHPO
ID_PNK1 SCHPO STANDARD; PRT; 421 AA.
AC O13911;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bifunctional polynucleotide phosphatase/kinase [Includes:
DE Polynucleotide 3'-phosphatase (EC 3.1.3.32) (2'(3')-polynucleotidase);
DE Polynucleotide 5'-hydroxyl-kinase (EC 2.7.1.78)].
GN PNK1 OR SPAC23C11.04C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=21683566; PubMed=11729194;
RA Meijer M., Karimi-Busheri F., Huang T.Y., Weinfeld M., Young D.;
RT "Pnk1, a DNA kinase/phosphatase required for normal response to DNA
RT damage by gamma-radiation or camptothecin in Schizosaccharomyces
RT pombe.";
RL J. Biol. Chem. 277:4050-4055(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
-!- FUNCTION: Has a role in the repair of breaks in single stranded
DNA.
-!- CATALYTIC ACTIVITY: 3'-phosphopolynucleotide + H(2)O =
polynucleotide + phosphate.
-!- CATALYTIC ACTIVITY: ATP + 5'-dephospho-DNA = ADP + 5'-phospho-DNA.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: TO HUMAN PNKP, C.ELEGANS F21D5.5, YEAST YMR156C AND
ACMNPV ORF33.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; Z98559; CAB11157.1; -.
PIR; T38242; T38242.
GeneDB SPombe; SPAC23C11.04C; -.
InterPro; IPR006551; DNA-3-Pase.
InterPro; IPR006549; HAD-SF-IIIA.
TIGRFAMS; TIGR01664; DNA-3-Pase; 1.
TIGRFAMS; TIGR01662; HAD-SF-IIIA; 1.
KW Multifunctional enzyme; Transferase; Kinase; Hydrolase; DNA repair;
ATP-binding; Nuclear protein.
FT NP BIND 263 270 ATP (POTENTIAL).
SQ SEQUENCE 421 AA; 48477 MW; FE9A732CD40E3146 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 421;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 93 ADWTW 97

RESULT 20
NRAM IAQIT
ID_NRAM IAQIT STANDARD; PRT; 470 AA.
AC Q07584;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Quail/Italy/1117/65).

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06587; AAA43373.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52005 MW; 9F743833EAC7F1C2 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 470;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||:|
Db 453 ADWTW 457

RESULT 21
BGLA_BACSU
ID BGLA_BACSU STANDARD; PRT; 479 AA.
AC P42973;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phospho-beta-glucosidase (EC 3.2.1.86).
GN BGLA OR BSU40110.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=168 / JH642;
RX MEDLINE=94171085; PubMed=8125345;
RA Zhang J., Aronson A.I.;
RT "A Bacillus subtilis bglA gene encoding phospho-beta-glucosidase is
RT inducible and closely linked to a NADH dehydrogenase-encoding gene.";
RL Gene 140:85-90(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
RT "36kb sequence between gnt2 and trnY of B. subtilis genome.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Chou S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucoside-(1,4)-D-glucose +
CC H(2)O = D-glucose 6-phosphate + D-glucose.
CC -!- SIMILARITY: Belongs to family 1 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L19710; AAA22660.1; -.
DR EMBL; D78193; BAA11270.1; -.
DR EMBL; D99124; CAB16048.1; -.
DR PIR; I39953; I39953.
DR HSSP; P11546; 1PBG.
DR Subtilist; BGI1203; bglA.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR ProDom; PD000650; Glyco_hydro_1; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
KW Hydrolase; Glycosidase; Complete proteome.
FT ACT_SITE 176 176 PROTON DONOR (POTENTIAL).


```
FT ACT SITE 377 377 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 479 AA; 54841 MW; FC9FA6131A14257A CRC64;

Query Match      82.5%; Score 33; DB 1; Length 479;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 ADWSWA 6
Db 347 SDWGWA 352

RESULT 22
AERA_AERTR STANDARD; PRT; 492 AA.
ID AERA_AERTR STANDARD; PRT; 492 AA.
AC P09166;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aerolysin precursor.
GN AERA.
OS Aeromonas trota.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29489;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB3;
RX MEDLINE=89013892; PubMed=2459581;
RA Husslein V., Huhle B., Jarchau T., Lurz R., Goebel W., Chakraborty T.;
RT "Nucleotide sequence and transcriptional analysis of the aerCaera
region of Aeromonas sobria encoding aerolysin and its regulatory
region.";
RL Mol. Microbiol. 2:507-517(1988).
CC -!- FUNCTION: Aerolysin is a cytolytic toxin exported by the Gram
negative Aeromonas bacteria. The mature toxin binds to eukaryotic
cells and aggregates to form holes approximately 3 nm in
diameter, leading to destruction of the membrane permeability
barrier and osmotic lysis (By similarity).
CC -!- SUBUNIT: Homodimer in solution; heptamer in the membrane (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the aerolysin family.
CC -!- CAUTION: Was originally thought to originate from A.sobria.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; Y00559; CAA68642.1; -.
DR HSSP; P09167; 1PRE.
DR InterPro; IPR005831; Aer_hem.
DR InterPro; IPR005830; Aer_hem_leuk.
DR InterPro; IPR005832; Aerolysin.
DR InterPro; IPR005138; APT.
DR Pfam; PF01117; Aerolysin; 1.
DR Pfam; PF03440; APT; 1.
DR PRINTS; PR00754; AEROLYSIN.
DR PROSITE; PS00274; AEROLYSIN; 1.
KW Hemolysis; Toxin; Membrane; Signal.
FT SIGNAL 1 21 AEROLYSIN.
FT CHAIN 22 445
FT PROPEP 446 492
FT DISULFID 42 98 BY SIMILARITY.
FT DISULFID 182 187 BY SIMILARITY.
SQ SEQUENCE 492 AA; 54493 MW; 520F25D2B6CA9A38 CRC64;

Query Match      82.5%; Score 33; DB 1; Length 492;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
```

```
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 395 DWNWA 399

RESULT 23
GUAA_MYCLE STANDARD; PRT; 529 AA.
ID GUAA_MYCLE STANDARD; PRT; 529 AA.
AC P46810; Q9CCU9;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine
amidotransferase) (GMP synthetase).
GN GUAA OR ML0395 OR B1620_C2_205.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +
H(2)O = AMP + diphosphate + GMP + L-glutamate.
CC -!- PATHWAY: GMP biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: In the C-terminal section; belongs to the GMP synthase
family.
CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; U00015; AAC43222.1; ALT_INIT.
DR EMBL; AL583918; CAC29903.1; -.
DR PIR; C86958; C86958.
DR HSSP; P04079; 1GPM.
DR Leproma; ML0395; -.
DR HAMAP; MF_00344; -.
DR InterPro; IPR006220; Anth_synthII.
DR InterPro; IPR001317; CP_synthGATase.
DR InterPro; IPR000991; GATase_1.
DR InterPro; IPR001674; GMP_synth_C.
DR InterPro; IPR004739; GMP_synth_N.
DR Pfam; PF00117; GATase; 1.
DR Pfam; PF00958; GMP_synt_C; 1.
DR PRINTS; PR00097; ANTSNTHASEII.
DR PRINTS; PR00099; CPSGATASE.
DR PRINTS; PR00096; GATASE.
DR TIGRFAMs; TIGR00884; guaA_Cterm; 1.
```


DR TIGRFAMs; TIGR00888; guaA Nterm; 1.
DR PROSITE; PS00442; GATASE TYPE I; 1.
KW Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
KW Glutamine amidotransferase; Complete proteome.
FT DOMAIN 1 204 GLUTAMINE AMIDOTRANSFERASE.
FT DOMAIN 237 404 GMP-BINDING (BY SIMILARITY).
FT ACT_SITE 93 GATASE (BY SIMILARITY).
FT ACT_SITE 179 193 GATASE (BY SIMILARITY).
FT ACT_SITE 181 181 GATASE (BY SIMILARITY).
FT NP_BIND 233 239 ATP (BY SIMILARITY).
SQ SEQUENCE 529 AA; 56723 MW; 443EDE9525CDD949 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 529;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 487 ADWTW 491

RESULT 24
YC20_METJA STANDARD; PRT; 578 AA.
AC Q586I7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1220.
GN MJ1220.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: TO M.JANNASCHII MJ0132 AND MJEC42.
CC -!- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES
(M SUBUNIT).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67563; AAB99225.1; -.
DR PIR; C64452; C64452.
DR TIGR; MJ1220; -.
DR InterPro; IPR003665; Methylase M.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR003356; N6_DNA_Mtase.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF02506; Methylase_M; 1.
DR Pfam; PF02384; N6_Mtase; 1.
DR PRINTS; PR00507; N12N6MTFRASE.
DR PROSITE; PS00092; N6_MTASE; 1.
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 578 AA; 66636 MW; 5339ED873EF8E9E2 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 578;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 391 ADWAW 395

RESULT 25
YC12_KLEPN STANDARD; PRT; 579 AA.
AC Q48458;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 65.4 kDa protein in cps region (ORF12).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Chedid;
RX MEDLINE=95204345; PubMed=7896702;
RA Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
RA Ohta M.;
RT "Genomic organization of the Klebsiella pneumoniae cps region
responsible for serotype K2 capsular polysaccharide synthesis in the
virulent strain Chedid.";
RL J. Bacteriol. 177:1788-1796(1995).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D21242; BAA04783.1; -.
DR KW Hypothetical protein.
SQ SEQUENCE 579 AA; 65385 MW; 7A8994B7590202DE CRC64;

Query Match 82.5%; Score 33; DB 1; Length 579;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 537 SDWSW 541

RESULT 26
PHK_STRCO STANDARD; PRT; 817 AA.
AC Q8CK51;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable phosphotetrolase (EC 4.1.2.-).
GN SCO0617 OR SCF56.01C OR SCF55.41C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,


```
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- COFACTOR: Thiamine pyrophosphate (Potential).
CC -!- SIMILARITY: Belongs to the XFP family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL939106; CAD55268.1; -.
DR HAMAP; MF_01403; -.
DR InterPro; IPR000399; Pyruvate_decarb.
DR InterPro; IPR005593; XFP.
DR Pfam; PF03894; XFP; 1.
DR PROSITE; PS60002; PHOSPHOKETOLASE_1; 1.
DR PROSITE; PS60003; PHOSPHOKETOLASE_2; 1.
DR PROSITE; PS00187; TPP ENZYMES; FALSE_NEG.
KW Lyase; Flavoprotein; Thiamine pyrophosphate; Complete proteome.
SQ SEQUENCE 817 AA; 90246 MW; ED489C3E63B31442 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 817;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 809 ADWTW 813

RESULT 27
GUX2_CLOSR STANDARD; PRT; 914 AA.
AC P50900;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Exoglucanase II precursor (EC 3.2.1.91) (Exocellobiohydrolase II)
DE (1,4-beta-cellobiohydrolase II) (Avicelase II).
GN CELY.
OS Clostridium stercorarium.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 11754;
RA Bronnenmeier K., Kuntz K., Riedel K., Schwarz W.H.,
RA Staudenbauer W.L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=NCIB 11754;
RX MEDLINE=91364686; PubMed=1909625;
RA Bronnenmeier K., Ruecknagel K.P., Staudenbauer W.L.;
RT "Purification and properties of a novel type of
RT exo-1,4-beta-glucanase (avicelase II) from the cellulolytic
RT thermophile Clostridium stercorarium.";
RL Eur. J. Biochem. 200:379-385(1991).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC in cellulose and cellotetraose, releasing cellobiose from the non-
```

```
CC reducing ends of the chains.
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL
CC HYDROLASES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z69359; CAA93280.1; -.
DR HSSP; Q06851; INBC.
DR InterPro; IPR001956; CBD_3.
DR InterPro; IPR008965; Cellul_bind.
DR InterPro; IPR005102; DUF291.
DR InterPro; IPR000556; Glyco_hydro_48.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00942; CBM_3; 1.
DR Pfam; PF03442; DUF291; 1.
DR Pfam; PF02011; Glyco_hydro_48; 1.
DR PRINTS; PR00844; GLHYDRLASE48.
DR ProDom; PD001947; CBD_3; 1.
DR ProDom; PD011903; Glyco_hydro_48; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 914 EXOGLUCANASE II.
SQ SEQUENCE 914 AA; 103020 MW; D0DB6017D6DFF82C CRC64;

Query Match 82.5%; Score 33; DB 1; Length 914;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 338 ADMAW 342

RESULT 28
NOS3_MOUSE STANDARD; PRT; 1201 AA.
ID P70313; O55056;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS).
GN NOS3 OR ECNOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal heart;
RX MEDLINE=96350460; PubMed=8764825;
RA Gnanapandithen K., Chen Z., Kau C.-L., Gorczynski R.M., Marsden P.A.;
RT "Cloning and characterization of murine endothelial constitutive
RT nitric oxide synthase.";
RL Biochim. Biophys. Acta 1308:103-106(1996).
RN [2]
RP SEQUENCE OF 1-53 FROM N.A.
RC TISSUE=Fetal heart;
RA Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.L., O'Brien W.E.;
RT "Limb reduction defects in endothelial nitric oxide synthase deficient
RT mice.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=99061722; PubMed=9843834;
RA Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.G.L., O'Brien W.E.;
```


RT "Limb reduction defects in endothelial nitric oxide synthase-deficient
RL mice."; Am. J. Physiol. 275:H2319-H2324(1998).
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets. May
CC play a significant role in normal and abnormal limb development.
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COPACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme.
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin (By
CC similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U53142; AAC52766.1; -.
DR EMBL; AF045940; AAC02553.1; -.
DR PIR; S71424; S71424.
DR HSSP; P29474; 3NOS.
DR MGD; MGI:97362; Nos3.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR008254; Flav_nitox synth.
DR InterPro; IPR001094; Flavodoxin_Like.
DR InterPro; IPR001709; FPN_cyt redctse.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
KW Lipoproteins; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
KW Multigene family.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 518 701 FLAVODOXIN-LIKE.
FT METAL 182 182 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT DOMAIN 489 508 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 647 678 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 791 802 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 933 943 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 1008 1026 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1106 1121 NADP (ADP PART) (BY SIMILARITY).
FT LIPID 1 1 N-myristoyl glycine (By similarity).
FT LIPID 14 14 S-palmitoyl cysteine (By similarity).
FT LIPID 25 25 S-palmitoyl cysteine (By similarity).
FT METAL 92 92 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT CONFLICT 49 49 A -> P (IN REF. 2).
SQ SEQUENCE 1201 AA; 132748 MW; DA37ABAC947DABD5 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 1201;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|

Db 441 ADWAW 445

RESULT 29
NOS3 HUMAN
ID NOS3_HUMAN STANDARD; PRT; 1202 AA.
AC P29474; Q13662; Q14251; Q14434;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS).
GN NOS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92340475; PubMed=1378832;
RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
RT "Cloning and expression of a cDNA encoding human endothelium-derived
RT relaxing factor/nitric oxide synthase.";
RL J. Biol. Chem. 267:14519-14522(1992).
RN [2]
RP ERRATUM.
RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
RL J. Biol. Chem. 267:22694-22694(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92354731; PubMed=1379542;
RA Marsden P.A., Schappert K.T., Chen H.S., Flowers M., Sundell C.L.,
RA Wilcox J.N., Lamas S., Michel T.;
RT "Molecular cloning and characterization of human endothelial nitric
RT oxide synthase.";
RL FEBS Lett. 307:287-293(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93352539; PubMed=7688726;
RA Marsden P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V.,
RA Shi X.-M., Tsui L.-C., Schappert K.T.;
RT "Structure and chromosomal localization of the human constitutive
RT endothelial nitric oxide synthase gene.";
RL J. Biol. Chem. 268:17478-17488(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RA Liao J.K.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94161710; PubMed=7509596;
RA Nadaud S.A., Bonnardeaux A., Lathrop M., Soubrier F.;
RT "Gene structure, polymorphism and mapping of the human endothelial
RT nitric oxide synthase gene.";
RL Biochem. Biophys. Res. Commun. 198:1027-1033(1994).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=94333373; PubMed=7519987;
RA Miyahara K., Kawamoto T., Sase K., Yui Y., Toda K., Yang L.X.,
RA Hattori R., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,
RA Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;
RT "Cloning and structural characterization of the human endothelial
RT nitric-oxide-synthase gene.";
RL Eur. J. Biochem. 223:719-726(1994).
RN [8]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 1-52 FROM N.A.

RC TISSUE=Placenta;
RX MEDLINE=94245207; PubMed=7514568;
RA Robinson L.J., Weremowicz S., Morton C.C., Michel T.;
RT "Isolation and chromosomal localization of the human endothelial
RL nitric oxide synthase (NOS3) gene.";
RL Genomics 19:350-357(1994).
RN [10]
RP SEQUENCE OF 410-527 FROM N.A.
RC TISSUE=Platelet;
RX MEDLINE=96077182; PubMed=7475956;
RA Sase K., Michel T.;
RT "Expression of constitutive endothelial nitric oxide synthase in human
RL blood platelets.";
RL Life Sci. 57:2049-2055(1995).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=99173237; PubMed=10074942;
RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
RA Weber P.C.;
RT "Structural characterization of nitric oxide synthase isoforms
RL reveals striking active-site conservation.";
RL Nat. Struct. Biol. 6:233-242(1999).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.96 ANGSTROMS) OF 66-479.
RX MEDLINE=22325496; PubMed=12437348;
RA Rosenfeld R.J., Garcia E.D., Panda K., Andersson G., Aberg A.,
RA Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,
RA Getzoff E.D.;
RT "Conformational changes in nitric oxide synthases induced by
RL chlorzoxazone and nitroindazoles: crystallographic and computational
RT analyses of inhibitor potency.";
RL Biochemistry 41:13915-13925(2002).
RN [13]
RP VARIANT SUSCEPTIBILITY TO CORONARY SPASM ASP-297.
RX MEDLINE=98407797; PubMed=9737779;
RA Yoshimura M., Yasue H., Nakayama M., Shimasaki Y., Sumida H.,
RA Sugiyama S., Kugiyama K., Ogawa H., Ogawa Y., Saito Y., Miyamoto Y.,
RA Nakao K.;
RT "A missense Glu298Asp variant in the endothelial nitric oxide synthase
RL gene is associated with coronary spasm in the Japanese.";
RL Hum. Genet. 103:65-69(1998).
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets.
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme.
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Platelets.
CC -!- POLYMORPHISM: Variation in NOS3 seem to be associated with
CC susceptibility to coronary spasm.
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC
CC EMBL; M93718; AAA36364.1; -.
CC EMBL; M95296; AAA36372.1; -.
CC EMBL; L10709; AAA36365.1; -.
CC EMBL; L10693; AAA36365.1; JOINED.
CC EMBL; L10694; AAA36365.1; JOINED.

DR EMBL; L10695; AAA36365.1; JOINED.
DR EMBL; L10696; AAA36365.1; JOINED.
DR EMBL; L10697; AAA36365.1; JOINED.
DR EMBL; L10698; AAA36365.1; JOINED.
DR EMBL; L10699; AAA36365.1; JOINED.
DR EMBL; L10700; AAA36365.1; JOINED.
DR EMBL; L10701; AAA36365.1; JOINED.
DR EMBL; L10702; AAA36365.1; JOINED.
DR EMBL; L10703; AAA36365.1; JOINED.
DR EMBL; L10704; AAA36365.1; JOINED.
DR EMBL; L10705; AAA36365.1; JOINED.
DR EMBL; L10706; AAA36365.1; JOINED.
DR EMBL; L10707; AAA36365.1; JOINED.
DR EMBL; L10708; AAA36365.1; JOINED.
DR EMBL; L26914; AAA36374.1; -.
DR EMBL; L26914; AAA36374.1; -.
DR EMBL; X76303; CAA53950.1; -.
DR EMBL; X76304; CAA53950.1; JOINED.
DR EMBL; X76305; CAA53950.1; JOINED.
DR EMBL; X76306; CAA53950.1; JOINED.
DR EMBL; X76307; CAA53950.1; JOINED.
DR EMBL; X76308; CAA53950.1; JOINED.
DR EMBL; X76309; CAA53950.1; JOINED.
DR EMBL; X76310; CAA53950.1; JOINED.
DR EMBL; X76311; CAA53950.1; JOINED.
DR EMBL; X76312; CAA53950.1; JOINED.
DR EMBL; X76313; CAA53950.1; JOINED.
DR EMBL; X76314; CAA53950.1; JOINED.
DR EMBL; X76315; CAA53950.1; JOINED.
DR EMBL; X76316; CAA53950.1; JOINED.
DR EMBL; D26607; BAA05652.1; -.
DR EMBL; AF519768; AAM74944.1; -.
DR EMBL; L23210; AAA36373.1; -.
DR EMBL; S80791; AAD14336.1; -.
DR PIR; A47501; A47501.
DR PDB; 3NOS; 04-FEB-00.
DR PDB; 1M9J; 11-DEC-02.
DR PDB; 1M9K; 11-DEC-02.
DR PDB; 1M9M; 11-DEC-02.
DR PDB; 1M9Q; 11-DEC-02.
DR PDB; 1M9R; 11-DEC-02.
DR Genew; HGNC:7876; NOS3.
DR MIM; 163729; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.

Query Match 82.5%; Score 33; DB 1; Length 1202;
Best Local Similarity 80.0%; Pred.No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:
Db 442 ADWAW 446

RESULT 30
NOS3_BOVIN
ID_NOS3_BOVIN STANDARD; PRT; 1204 AA.
AC P29473;

DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS).
GN NOS3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=923335295; PubMed=1378626;
RX Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;
RA "Endothelial nitric oxide synthase: molecular cloning and
RT characterization of a distinct constitutive enzyme isoform.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=93055452; PubMed=1385480;
RA Nishida K., Harrison D.G., Navas J.P., Fisher A.A., Dockery S.P.,
RA Uematsu M., Nerem R.M., Alexander R.W., Murphy T.J.;
RT "Molecular cloning and characterization of the constitutive bovine
RT aortic endothelial cell nitric oxide synthase.";
RL J. Clin. Invest. 90:2092-2096(1992).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RX MEDLINE=92348367; PubMed=1379225;
RA Sessa W.C., Harrison J.K., Barber C.M., Zeng D., Durieux M.E.,
RA D'Angelo D.D., Lynch K.R., Peach M.J.;
RT "Molecular cloning and expression of a cDNA encoding endothelial cell
RT nitric oxide synthase.";
RL J. Biol. Chem. 267:15274-15276(1992).
RN [4]
RN MYRISTOYLATION.
RX MEDLINE=93231982; PubMed=7682550;
RA Busconi L., Michel T.;
RT "Endothelial nitric oxide synthase. N-terminal myristoylation
RT determines subcellular localization.";
RL J. Biol. Chem. 268:8410-8413(1993).
RN [5]
RN PALMITOYLATION.
RX MEDLINE=96102197; PubMed=8524847;
RA Robinson L.J., Michel T.;
RT "Mutagenesis of palmitoylation sites in endothelial nitric oxide
RT synthase identifies a novel motif for dual acylation and subcellular
RT targeting.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11776-11780(1995).
RN [6]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 66-481.
RX MEDLINE=99091052; PubMed=9875848;
RA Raman C.S., Li H., Martasek P., Kral V., Masters B.S.S., Poulos T.L.;
RT "Crystal structure of constitutive endothelial nitric oxide synthase:
RT a paradigm for pterin function involving a novel metal center.";
RL Cell 95:939-950(1998).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS) OF 66-481.
RX MEDLINE=20503854; PubMed=11051558;
RA Li H., Raman C.S., Martasek P., Kral V., Masters B.S.S., Poulos T.L.;
RT "Mapping the active site polarity in structures of endothelial
RT nitric oxide synthase heme domain complexed with isothioureas.";
RL J. Inorg. Biochem. 81:133-139(2000).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).
RX MEDLINE=21229525; PubMed=11331003;
RA Li H., Raman C.S., Martasek P., Masters B.S.S., Poulos T.L.;
RT "Crystallographic studies on endothelial nitric oxide synthase
RT complexed with nitric oxide and mechanism-based inhibitors.";
RL Biochemistry 40:5399-5406(2001).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=21552923; PubMed=11695891;
RA Raman C.S., Li H., Martasek P., Southan G., Masters B.S.S.,
RA Poulos T.L.;
RT "Crystal structure of nitric oxide synthase bound to nitro indazole
RT reveals a novel inactivation mechanism.";
RL Biochemistry 40:13448-13455(2001).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).
RX MEDLINE=21336567; PubMed=11331290;
RA Raman C.S., Li H., Martasek P., Babu B.R., Griffith O.W., Southan G.,
RA Masters B.S.S., Poulos T.L.;
RT "Implications for isoform-selective inhibitor design derived from the
RT binding mode of bulky isothioureas to the heme domain of endothelial
RT nitric-oxide synthase.";
RL J. Biol. Chem. 276:26486-26491(2001).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS).
RX MEDLINE=21623579; PubMed=11590164;
RA Kotsonis P., Frohlich L.G., Raman C.S., Li H., Berg M., Gerwig R.,
RA Groehn V., Kang Y., Al-Masoudi N., Taghavi-Moghadam S., Mohr D.,
RA Munch U., Schnabel J., Martasek P., Masters B.S.S., Strobel H.,
RA Poulos T., Matter H., Pfeleiderer W., Schmidt H.H.H.W.;
RT "Structural basis for pterin antagonism in nitric-oxide synthase.
RT Development of novel 4-oxo-pteridine antagonists of
RT (6R)-5,6,7,8-tetrahydrobiopterin.";
RL J. Biol. Chem. 276:49133-49141(2001).
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets.
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme.
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M99057; AAA30667.1; -.
DR EMBL; M89952; AAA30494.1; -.
DR EMBL; M95674; AAA30669.1; -.
DR PIR; A38943; A38943.
DR PDB; 1NSE; 18-MAY-99.
DR PDB; 2NSE; 25-MAY-99.
DR PDB; 3NSE; 18-MAY-99.
DR PDB; 4NSE; 18-MAY-99.
DR PDB; 8NSE; 21-NOV-01.
DR PDB; 9NSE; 25-OCT-00.
DR PDB; 1D1W; 25-OCT-00.
DR PDB; 1ED4; 25-OCT-00.
DR PDB; 1DM6; 21-NOV-01.
DR PDB; 1DM7; 13-DEC-00.
DR PDB; 1DM8; 13-DEC-00.
DR PDB; 1DMI; 20-DEC-00.
DR PDB; 1DMJ; 04-JAN-01.
DR PDB; 1ED5; 12-DEC-01.
DR PDB; 1ED6; 08-AUG-01.
DR PDB; 1FOI; 20-JUL-01.
DR PDB; 1FOL; 20-JUL-01.
DR PDB; 1FOO; 20-JUL-01.
DR PDB; 1FOP; 20-JUL-01.
DR PDB; 1D1V; 25-JUL-01.

FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 100 100 ZINC (BY SIMILARITY).
SQ SEQUENCE 1204 AA; 133274 MW; 48676BA95D814CFE CRC64;

Query Match 82.5%; Score 33; DB 1; Length 1204;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 444 ADWAW 448

RESULT 32
ID_NOS3_CAVPO STANDARD; PRT; 100 AA.
AC P97270;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).
DE (Fragment).
GN NOS3 OR ENOS.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=99057793; PubMed=9838160;
RA Aguan K., Murotsuki J., Gagnon R., Thompson L.P., Weiner C.P.;
RT "Effect of chronic hypoxemia on the regulation of nitric-oxide synthase in the fetal sheep brain."
RL Brain Res. Dev. Brain Res. 111:271-277(1998).
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. No mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets (By similarity).
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- INDUCTION: Repressed by hypoxemia in fetal brain.
CC -!- SIMILARITY: Belongs to the NOS family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U76736; AAB40703.1; -.
DR HSSP; P29474; 3NOS.
DR InterPro; IPR004030; NO_synthase.
DR Pfam; PF02898; NO_synthase; 1.
DR PROSITE; PS60001; NOS; PARTIAL.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding; Heme; Multigene family.
FT NON_TER 1
FT NON_TER 100
SQ SEQUENCE 100 AA; 11271 MW; 867D7F89F4B132A8 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 100;

Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 88 ADWGW 92

RESULT 33
ID_STEL_RHUVE STANDARD; PRT; 107 AA.
AC P00302;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Stellacyanin.
OS Rhus vernicifera (Japanese lacquer tree) (Varnish tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Sapindales; Anacardiaceae; Toxicodendron.
OX NCBI_TaxID=4013;
RN [1]
RP SEQUENCE.
RX MEDLINE=77266668; PubMed=901509;
RA Bergman C., Gandvik E.K., Nyman P.O., Strid L.;
RT "The amino acid sequence of stellacyanin from the lacquer tree."
RL Biochem. Biophys. Res. Commun. 77:1052-1059(1977).
RN [2]
RP ERRATUM.
RA Bergman C., Gandvik E.K., Nyman P.O., Strid L.;
RL Biochem. Biophys. Res. Commun. 79:1013-1013(1977).
RN [3]
RP DISULFIDE BOND.
RX MEDLINE=84208877; PubMed=6723985;
RA Engeseth H.R., Hermodson M.A., McMillin D.R.;
RT "A new assignment of the disulfide linkage in stellacyanin."
RL FEBS Lett. 171:257-261(1984).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=92106330; PubMed=1762145;
RA Fields B.A., Guss J.M., Freeman H.C.;
RT "Three-dimensional model for stellacyanin, a 'blue' copper-protein."
RL J. Mol. Biol. 222:1053-1065(1991).
CC -!- FUNCTION: The midpoint redox potential is +184 mV.
CC -!- SIMILARITY: Contains 1 plastocyanin-like domain.
DR PIR; A00311; SSUL.
DR HSSP; P00303; 2CBP.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR003245; Plcyanin_like.
DR Pfam; PF02298; Cu_bind_like; 1.
DR ProDom; PD003122; Plcyanin_like; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
KW Electron transport; Copper; Glycoprotein.
FT DOMAIN 1 107 PLASTOCYANIN-LIKE.
FT DISULFID 59 93
FT METAL 46 46 COPPER.
FT METAL 87 87 COPPER.
FT METAL 92 92 COPPER.
FT METAL 97 97 COPPER.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 107 AA; 12296 MW; 4AF450E1A0461069 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 107;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 22 DWKWA 26


```

RESULT 34
VG61_BPMD2
ID_VG61_BPMD2 STANDARD; PRT; 125 AA.
AC O64253;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Gene 61 protein (GP61).
GN 61.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: implications for phage evolution.";
RL J. Mol. Biol. 279:143-164(1998).
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; AF022214; AAC18503.1; -.
PIR; D72807; D72807.
SEQUENCE 125 AA; 14029 MW; 38BA367ADBBC19F9 CRC64;
-----
Query Match 80.0%; Score 32; DB 1; Length 125;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
-----
QY 1 ADWSW 5
Db 68 ADWEW 72
-----
RESULT 35
CY1_RHORU
ID_CY1_RHORU STANDARD; PRT; 272 AA.
AC P23135;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c1 precursor.
GN P2C.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-50.
RX STRAIN=FR1;
RA Majewski C., Trebst A.;
RT "The pet genes of Rhodospirillum rubrum: cloning and sequencing of the genes for the cytochrome b-c1 complex.";
RL Mol. Gen. Genet. 224:373-382(1990).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis.
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
```

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; X55387; CAA39060.1; -.
PIR; S12258; CCQFLR.
InterPro; IPR002326; Cyt C1.
InterPro; IPR000345; CytC_heme_BS.
Pfam; PF02167; Cytochrome_C1; 1.
PRINTS; PR00603; CYTOCHROME_C1.
PROSITE; PS00190; CYTOCHROME_C; 1.
Electron transport; Respiratory chain; Heme; Transmembrane; Signal.
FT SIGNAL 1 24
FT CHAIN 25 272 CYTOCHROME C1.
FT BINDING 61 61 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 64 64 HEME (COVALENT) (BY SIMILARITY).
FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 200 200 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT TRANSMEM 244 261 ANCHORS TO THE MEMBRANE (POTENTIAL).
FT SEQUENCE 272 AA; 29494 MW; D2575CEBE7CC9332 CRC64;
-----
Query Match 80.0%; Score 32; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-----
QY 2 DWSW 5
Db 35 DWSW 38
-----
RESULT 36
3MG2_ECOLI
ID_3MG2_ECOLI STANDARD; PRT; 282 AA.
AC P04395;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-3-methyladenine glycosylase II (EC 3.2.2.21) (3-methyladenine-DNA glycosylase II, inducible) (TAG II) (DNA-3-methyladenine glycosidase II).
GN ALKA OR AIDA OR B2068.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-12 AND 14-20.
RX MEDLINE=85054800; PubMed=6094528;
RA Nakabeppu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;
RT "Structure and expression of the alka gene of Escherichia coli involved in adaptive response to alkylating agents.";
RL J. Biol. Chem. 259:13730-13736(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
```


RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=85054799; PubMed=6389535;
RA Nakabeppu Y., Kondo H., Sekiguchi M.;
RT "Cloning and characterization of the alkA gene of Escherichia coli
RT that encodes 3-methyladenine DNA glycosylase II.";
RL J. Biol. Chem. 259:13723-13729(1984).
RN [5]
RP SEQUENCE OF 1-2 FROM N.A.
RX MEDLINE=86313568; PubMed=3529081;
RA Nakabeppu Y., Sekiguchi M.;
RT "Regulatory mechanisms for induction of synthesis of repair enzymes
RT in response to alkylating agents: ada protein acts as a
RT transcriptional regulator.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6297-6301(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS), AND MUTAGENESIS.
RX MEDLINE=96319733; PubMed=8706135;
RA Yamagata Y., Kato M., Odawara K., Tokuno Y., Nakashima Y.,
RA Matsushima N., Yasumura K., Tomita K.-I., Ihara K., Fujii Y.,
RA Nakabeppu Y., Sekiguchi M., Fujii S.;
RT "Three-dimensional structure of a DNA repair enzyme, 3-methyladenine
RT DNA glycosylase II, from Escherichia coli.";
RL Cell 86:311-320(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=96319734; PubMed=8706136;
RA Labahn J., Scharer O.D., Long A., Ezaz-Nikpay K., Verdine G.L.,
RA Ellenberger T.E.;
RT "Structural basis for the excision repair of alkylation-damaged DNA.";
RL Cell 86:321-329(1996).
CC -1- FUNCTION: HYDROLYSIS OF THE DEOXYRIBOSE N-GLYCOSIDIC BOND TO
CC EXCISE 3-METHYLADENINE, 3-METHYLGUANINE, 7-METHYLGUANINE,
CC O2-METHYLTHYMINE, AND O2-METHYLCYTOSINE FROM THE DAMAGED DNA
CC POLYMER FORMED BY ALKYLATION LESIONS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alkylated DNA, releasing 3-
CC methyladenine, 3-methylguanaine, 7-methylguanaine, and 7-
CC methyladenine.
CC -1- SUBUNIT: Monomer.
CC -1- INDUCTION: WHEN E.COLI CELLS ARE EXPOSED TO DOSES OF DNA
CC ALKYLATING AGENT. IT IS NOT INHIBITED BY REACTION PRODUCTS.
CC -1- SIMILARITY: Belongs to the alkylbase DNA glycosidase alka family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02498; AAA23430.1; -.
DR EMBL; AE000297; AAC75129.1; -.
DR EMBL; D90844; BAA15921.1; -.
DR EMBL; D90845; BAA15926.1; -.
DR EMBL; M13827; -; NOT_ANNOTATED_CDS.
DR PIR; A00904; DGECEMA.
DR PDB; 1MPG; 28-JAN-98.
DR PDB; 1DIZ; 20-JUN-00.
DR EcoGene; EG11222; alka.
DR InterPro; IPR000035; AlbdNA_glycsylse.
DR InterPro; IPR003265; Endo_3c.
DR Pfam; PF00730; HhH-GPD; 1.
DR SMART; SM00478; ENDO3C; 1.
DR PROSITE; PS00516; ALKYLBASE_DNA_GLYCOS; 1.
KW DNA repair; Hydrolase; 3D-structure; Complete proteome.
FT SITE 218 218 DETERMINANT FOR SUBSTRATE SPECIFICITY
FT AND/OR ACTIVITY.
FT ACT SITE 238 238 PROTON ACCEPTOR.
FT MUTAGEN 124 124 Q->A: METHYLMETHANE SULFONATE-RESISTANT.

FT MUTAGEN 218 218 W->A: NO CATALYTIC ACTIVITY,
FT METHYLMETHANE SULFONATE-SENSITIVE.
FT MUTAGEN 237 237 D->N: MORE THAN 30% CATALYTIC ACTIVITY,
FT METHYLMETHANE SULFONATE-RESISTANT.
FT MUTAGEN 238 238 D->N: NO CATALYTIC ACTIVITY,
FT METHYLMETHANE SULFONATE-SENSITIVE.
FT STRAND 2 5
FT HELIX 12 22
FT TURN 25 27
FT STRAND 28 30
FT STRAND 35 41
FT TURN 42 43
FT STRAND 44 53
FT TURN 54 57
FT STRAND 58 63
FT HELIX 65 70
FT HELIX 71 82
FT TURN 83 85
FT HELIX 88 95
FT TURN 96 99
FT TURN 100 101
FT TURN 103 104
FT HELIX 113 122
FT TURN 123 125
FT HELIX 128 142
FT STRAND 145 145
FT TURN 150 151
FT STRAND 153 153
FT HELIX 158 162
FT TURN 163 163
FT HELIX 166 171
FT TURN 172 173
FT HELIX 176 191
FT TURN 192 192
FT HELIX 202 209
FT TURN 210 211
FT TURN 213 214
FT HELIX 217 227
FT TURN 236 237
FT HELIX 239 244
FT TURN 246 247
FT HELIX 250 257
FT HELIX 258 260
FT TURN 261 262
FT HELIX 264 272
FT TURN 273 273
FT TURN 275 276
SQ SEQUENCE 282 AA; 31393 MW; B66BB5E23019899C CRC64;
Query Match 80.0%; Score 32; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWSW 5
Db 11 DWSW 14
RESULT 37
X769 HUMAN
ID_X769_HUMAN STANDARD; PRT; 295 AA.
AC Q99871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE X-linked protein STS1769.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;

RX MEDLINE=97254469; PubMed=9099879;
RA Esposito T., Ciccodicola A., Flagiello L., Matarazzo M.R.,
RA Migliaccio C., Cifarelli R.A., Visone R., Campanile C.,
RA Mazzarella R., Schlessinger D., D'Urso M., D'Esposito M.;
RT "Expressed STSs and transcription of human Xq28.";
RL Gene 187:185-191(1997).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X99270; CAA67665.1; -.
DR Genew; HGNC:12270; TREX2.
DR InterPro; IPR003010; Ntlse/CNhydtse.
SQ SEQUENCE 295 AA; 33582 MW; 079BD40D8A56F45E CRC64;

Query Match 80.0%; Score 32; DB 1; Length 295;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 241 DWQWA 245

RESULT 38
YJGB_ECOLI
ID YJGB_ECOLI STANDARD; PRT; 339 AA.
AC P27250; P76812;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical zinc-type alcohol dehydrogenase-like protein YJGB.
GN YJGB OR B4269.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B;
RA Pucci M.J., Discotto L.F., Dougherty T.J.;
RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
CC -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M96355; AAA72122.1; -.
DR EMBL; U14003; AAA97166.1; ALT_INIT.
DR EMBL; AE000497; AAC77226.1; ALT_INIT.
DR EcoGene; EGI1436; YJGB.
DR InterPro; IPR002328; ADH_zinc.

DR InterPro; IPR002085; Adh zn family.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Hypothetical protein; Oxidoreductase; Zinc; Metal-binding;
KW Complete proteome.
FT METAL 38 38 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 63 63 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 96 96 ZINC 2 (BY SIMILARITY).
FT METAL 99 99 ZINC 2 (BY SIMILARITY).
FT METAL 102 102 ZINC 2 (BY SIMILARITY).
FT METAL 110 110 ZINC 2 (BY SIMILARITY).
FT METAL 152 152 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT CONFLICT 331 339 YRVVLKADF -> TAWC (IN REF. 1).
SQ SEQUENCE 339 AA; 36502 MW; 0854DDEFA16B9EEE CRC64;

Query Match 80.0%; Score 32; DB 1; Length 339;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 130 ADQWQ 134

RESULT 39
WNT2_CAEEL
ID WNT2_CAEEL STANDARD; PRT; 360 AA.
AC P34889;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Wnt-2 protein precursor.
GN WNT-2 OR CWN-2 OR W01B6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93288400; PubMed=8510930;
RA Shackleford G.M., Shivakumar S., Shiue L., Mason J., Kenyon C.,
RA Varmus H.E.;
RT "Two wnt genes in Caenorhabditis elegans.";
RL Oncogene 8:1857-1864(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Coles L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probable developmental protein. May be a
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- DEVELOPMENTAL STAGE: DETECTED IN ALL LARVAL FORMS AND ADULTS,
CC BUT IS MOST ABUNDANT IN THE EMBRYONIC STAGE.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X72943; CAA51448.1; -.
DR EMBL; Z68301; CAA92624.1; -.
DR PIR; S32695; S32695.
DR PIR; T26037; T26037.


```
DR WormPep; W01B6.1; CE03753.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR005816; wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 37
FT CHAIN 38 360
FT CARBOHYD 90 90
FT CARBOHYD 352 352
FT CONFLICT 73 73
FT CONFLICT 186 186
FT CONFLICT 221 221
FT CONFLICT 229 230
FT CONFLICT 333 333
SQ SEQUENCE 360 AA; 40551 MW; E4A6EAF82A710F46 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
Db 152 DWSW 155

RESULT 40
DCUP YEAST
ID DCUP YEAST STANDARD; PRT; 362 AA.
AC P32347;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
GN HEM12 OR HEM6 OR POP3 OR YD9609.03.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92249304; PubMed=1576986;
RA Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,
RA Kushner J., Labbe P.;
RT "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12
RT gene sequence and evidence for two conserved glycines essential for
RT enzymatic activity.";
RL Eur. J. Biochem. 205:1011-1016(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93348774; PubMed=8346678;
RA Diflumeri C., Larocque R., Keng T.;
RT "Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the
RT gene for uroporphyrinogen decarboxylase.";
RL Yeast 9:613-623(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP MUTANTS.
RX MEDLINE=93111946; PubMed=1471989;
RA Chelstowska A., Zoadek T., Garey J.R., Kushner J., Rytka J.,
RA Labbe-Bois R.;
RT "Identification of amino acid changes affecting yeast
RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12
RT mutant alleles.";
RL Biochem. J. 288:753-757(1992).
CC -!- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
CO(2).
```

```
CC -!- PATHWAY: Porphyrin and heme biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the uroporphyrinogen decarboxylase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X63721; CAA45253.1; -.
DR EMBL; Z19089; CAA79514.1; -.
DR EMBL; Z49209; CAA89078.1; -.
DR PIR; S23471; S23471.
DR HSSP; P06132; IURO.
DR Germonline; 140538; -.
DR SGD; S0002454; HEM12.
DR GO; GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.
DR GO; GO:0006783; P:heme biosynthesis; IMP.
DR InterPro; IPR006361; HemeE.
DR InterPro; IPR000257; Uro_decarbxylys.
DR Pfam; PF01208; URO-D; 1.
DR ProDom; PD003225; Uro_decarbxylys; 1.
DR TIGRFAMs; TIGR01464; hemeE; 1.
DR PROSITE; PS00906; UROD_1; 1.
DR PROSITE; PS00907; UROD_2; 1.
KW Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
FT VARIANT 59 59 S -> F (IN HEM12-6 AND HEM12-12).
FT VARIANT 62 62 T -> I (IN HEM12-14).
FT VARIANT 107 107 L -> S (IN HEM12-3 AND HEM12-13).
FT VARIANT 215 215 S -> N (IN HEM12-2 AND HEM12-11).
FT MUTAGEN 33 33 G->D: INACTIVATION.
FT MUTAGEN 300 300 G->D: INACTIVATION.
SQ SEQUENCE 362 AA; 41349 MW; E5CB3A48E62BC277 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
Db 280 DWSW 283

RESULT 41
HIS7_XANCP
ID HIS7_XANCP STANDARD; PRT; 375 AA.
AC P58882;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidine biosynthesis bifunctional protein hisB [includes:
DE Histidinol-phosphatase (EC 3.1.3.15); Imidazoleglycerol-phosphate
DE dehydratase (EC 4.2.1.19) (IGPD)].
GN HISB OR XCC1811.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
```


RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
CC -!- CATALYTIC ACTIVITY: D-erythro-1-(imidazol-4-yl)glycerol 3-
CC phosphate = 3-(imidazol-4-yl)-2-oxopropyl phosphate + H(2)O.
CC -!- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)O = L-histidinol
CC + phosphate.
CC -!- PATHWAY: Histidine biosynthesis; sixth step.
CC -!- PATHWAY: Histidine biosynthesis; eighth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: In the N-terminal section; belongs to the histidinol-
CC phosphatase family.
CC -!- SIMILARITY: In the C-terminal section; belongs to the
CC imidazoleglycerol-phosphate dehydratase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE012283; AAM41100.1; --
DR HAMAP; MF 01022; --; 1.
DR InterPro; IPR006549; HAD-SF-IIIa.
DR InterPro; IPR005954; HisB_N.
DR InterPro; IPR006543; Histidinol-phos.
DR InterPro; IPR000807; IGPD.
DR Pfam; PF00475; IGPD; 1.
DR ProDom; PD002282; IGPD; 1.
DR TIGRFAMS; TIGR01662; HAD-SF-IIIa; 1.
DR TIGRFAMS; TIGR01261; HisB_Nterm; 1.
DR TIGRFAMS; TIGR01656; Histidinol-ppas; 1.
DR PROSITE; PS00954; IGP_DEHYDRATASE_1; 1.
DR PROSITE; PS00955; IGP_DEHYDRATASE_2; 1.
KW Histidine biosynthesis; Multifunctional enzyme; Lyase; Hydrolase;
KW Complete proteome.
FT DOMAIN 1 168 HISTIDINOL-PHOSPHATASE.
FT DOMAIN 169 375 IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE.
SQ SEQUENCE 375 AA; 41812 MW; 758A9F43F0F5AF72 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 375;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 154 DWDWA 158

RESULT 42
FOLC_BUCAI
ID FOLC_BUCAI STANDARD; PRT; 411 AA.
AC P57265;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE FOLC bifunctional protein [Includes: Folylpolyglutamate synthase
DE (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS);
DE Dihydrofolate synthase (EC 6.3.2.12)].
DE FOLC OR BU167.
GN Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.

OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: Conversion of folates to polyglutamate derivatives.
CC -!- CATALYTIC ACTIVITY: ATP + {tetrahydrofolyl-[Glu]}(N) + L-glutamate
CC = ADP + phosphate + {tetrahydrofolyl-[Glu]}(N+1).
CC -!- CATALYTIC ACTIVITY: ATP + dihydropterate + L-glutamate = ADP +
CC phosphate + dihydrofolate.
CC -!- PATHWAY: Folate biosynthesis.
CC -!- SIMILARITY: Belongs to the folylpolyglutamate synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP001118; BAB12885.1; --
DR HSSP; P15925; lFGS.
DR InterPro; IPR001645; Fpolygl_synthtse.
DR InterPro; IPR000713; Mur_ligase.
DR Pfam; PF01225; Mur_ligase; 1.
DR TIGRFAMS; TIGR01499; folC; 1.
DR PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; 1.
DR PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; FALSE_NEG.
KW Multifunctional enzyme; Ligase; One-carbon metabolism; ATP-binding;
KW Folate biosynthesis; Complete proteome.
FT NP BIND 50 56 ATP (BY SIMILARITY).
SQ SEQUENCE 411 AA; 46970 MW; 5DDC2DC66539935A CRC64;

Query Match 80.0%; Score 32; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 220 DWSW 223

RESULT 43
HLT_VIBPA
ID HLT_VIBPA STANDARD; PRT; 418 AA.
AC Q99289;
DT 01-FEB-1995 (Rel. 31, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thermolabile hemolysin precursor (TL) (lecithin-dependent haemolysin)
DE (LDH) (Atypical phospholipase) (Phospholipase A2) (lysophospholipase).
GN VPA0226.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89237825; PubMed=3508495;
RA Taniguchi H., Hirano H., Kubomura S., Higashi K., Mizuguchi Y.;
RT "Comparison of the nucleotide sequences of the genes for the
RT thermostable direct hemolysin and the thermolabile hemolysin from
RT Vibrio parahaemolyticus";
RT Microb. Pathog. 1:425-432(1986).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=RIMD 2210633 / Serotype O3:K6;
RC MEDLINE=22508454; PubMed=12620739;
RX


```
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
[3]
RN SEQUENCE OF 20-47, AND CHARACTERIZATION.
RX MEDLINE=92166705; PubMed=1791426;
RA Shinoda S., Matsuoka H., Tauchie T., Miyoshi S.-I., Yamamoto S.,
RA Taniguchi H., Mizuguchi Y.;
RT "Purification and characterization of a lecithin-dependent haemolysin
RT from Escherichia coli transformed by a Vibrio parahaemolyticus
RT gene.";
RL J. Gen. Microbiol. 137:2705-2711(1991).
CC -|- FUNCTION: Phospholipase hydrolyzing both fatty acid esters of
CC phospholipid, i.e., it hydrolyzes phosphatidylcholine (PC) to
CC lysophosphatidylcholine (LPC) and then LPC to
CC glycerophosphorylcholine (GPC).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- PTM: There are two forms of LDH. The LDH(S) may be a protein in
CC which 13 residues of the N-terminal of LDH(L) are deleted.
CC -|- SIMILARITY: Belongs to the "GDSL" family of lipolytic enzymes.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M36437; AAA27526.1; -.
DR EMBL; AP005084; BAC61569.1; -.
DR PIR; A53888; A53888.
DR InterPro; IPR001087; Lipase_GDSL.
DR InterPro; IPR008265; Lipase_GDSL_AS.
DR Pfam; PF00657; Lipase_GDSL; 1.
DR PROSITE; PS01098; LIPASE_GDSL_SER; 1.
KW Hydrolase; Lipid degradation; Hemolysis; Toxin; Signal;
KW Complete proteome.
FT SIGNAL 1 19
FT CHAIN 20 418 THERMOLABILE HEMOLYSIN.
FT ACT_SITE 153 153 BY SIMILARITY.
FT ACT_SITE 395 395 POTENTIAL.
FT VARIANT 20 32 MISSING (IN LDH(S)).
FT CONFLICT 20 20 E -> T (IN REF. 3).
FT CONFLICT 219 219 E -> D (IN REF. 1).
FT CONFLICT 390 390 D -> N (IN REF. 1).
SQ SEQUENCE 418 AA; 47392 MW; DC59A641DD04B1BD CRC64;

Query Match 80.0%; Score 32; DB 1; Length 418;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 63 DWEWA 67

RESULT 44
NRAM_IAWIL
ID_NRAM_IAWIL STANDARD; PRT; 453 AA.
AC P03470;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Wilson-Smith/33).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11487;
```

```
RN SEQUENCE FROM N.A.
RP MEDLINE=82192605; PubMed=7077751;
RA Hiti A.L., Nayak D.P.;
RT "Complete nucleotide sequence of the neuraminidase gene of human
RT influenza virus A/WSN/33.";
RL J. Virol. 41:730-734(1982).
CC -|- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -|- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -|- SUBUNIT: Homotetramer.
CC -|- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -|- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02177; AAA43397.1; ALT_SEQ.
DR HSSP; P03472; 2QWC.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 35 ANCHOR.
FT DOMAIN 36 74 HYPERVARIABLE STALK REGION.
FT DOMAIN 75 453 HEAD OF NEURAMINIDASE.
FT ACT_SITE 259 259 PROBABLE.
FT ACT_SITE 261 261 PROBABLE.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 453 AA; 49623 MW; 7DC56A4416A47BE8 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
Db 438 DWSW 441

RESULT 45
NRAM_IAPUE
ID_NRAM_IAPUE STANDARD; PRT; 454 AA.
AC P03468;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Puerto Rico/8/34).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11455;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81148841; PubMed=7010182;
RA Fields S., Winter G., Brownlee G.G.;
RT "Structure of the neuraminidase gene in human influenza virus
RT A/PR/8/34.";
```


RL Nature 290:213-217(1981).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J02146; AAA43412.1; -.
CC HSSP; P03472; 2QCW.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM 7 35
CC DOMAIN 36 75
CC DOMAIN 76 454
CC ACT_SITE 260 260
CC ACT_SITE 262 262
CC CARBOHYD 44 44
CC CARBOHYD 58 58
CC CARBOHYD 73 73
CC CARBOHYD 131 131
CC CARBOHYD 220 220
CC SEQUENCE 454 AA; 50143 MW; A0DC4C08A2B53705 CRC64;
CC

Query Match 80.0%; Score 32; DB 1; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSW 5
Db 439 DWSW 442

RESULT 46
NOS2_ONCMY STANDARD; PRT; 470 AA.
ID NOS2_ONCMY
AC Q92091;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (INOS) (Fragment).
GN NOS2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Grabowski P.S., Laing K.J., Hardie L., Macguigan F., Ralston S.,
RA Secombes C.J.;
RT "Detection of mRNA for a nitric oxide synthase in macrophages and
RT gill of rainbow trout challenged with an attenuated bacterial
RT pathogen.";
RL (In) Moncada S., Stamler J., Gross S., Higgs E.A. (eds.);
RL 4th International meeting on the biology of nitric oxide, Amelia

RL Island, Florida, Sep. 1995, pp.10:48-48, Portland Press,
RL Brookfield (1996).
CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
CC with diverse functions throughout the body. In macrophages, NO
CC mediates tumoricidal and bactericidal actions.
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme (By similarity).
CC -!- ENZYME REGULATION: Not stimulated by calcium/calmodulin (By
CC similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X97013; CAA65736.1; -.
CC HSSP; P29477; INOS.
CC InterPro; IPR003097; FAD_binding.
CC InterPro; IPR008254; Flav_nitox_synth.
CC InterPro; IPR001094; Flavodoxin_Like.
CC InterPro; IPR004030; NO_synthase.
CC Pfam; PF00667; FAD_binding_1; 1.
CC Pfam; PF00258; flavodoxin; 1.
CC Pfam; PF02898; NO_synthase; 1.
CC PRINTS; PR00369; FLAVODOXIN.
CC PROSITE; PS50902; FLAVODOXIN LIKE; 1.
CC PROSITE; PS60001; NOS; PARTIAL.
CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme.
CC NON_TER 1 1
CC DOMAIN 139 159 CALMODULIN-BINDING (POTENTIAL).
CC DOMAIN 169 307 FLAVODOXIN-LIKE.
CC NP_BIND 253 284 FMN (PYRIMIDINE PART) (BY SIMILARITY).
CC NP_BIND 398 409 FAD (ADP PART) (BY SIMILARITY).
CC NON_TER 470 470
CC SEQUENCE 470 AA; 53329 MW; 40B6717EE500B64D CRC64;
CC

Query Match 80.0%; Score 32; DB 1; Length 470;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 89 ADWDW 93

RESULT 47
ENGA_BRUME STANDARD; PRT; 483 AA.
ID ENGA_BRUME
AC Q8YFH2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE GTP-binding protein engA.
GN ENGA OR BMEI1550.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyripides N., Overbeek R.,
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: GTPase of unknown physiological role.
CC -!- SIMILARITY: Belongs to the era/trmE family of GTP-binding
CC proteins. EngA subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE009590; AAL52731.1; -.
DR PIR; AH3445; AH3445.
DR HAMAP; MF 00195; -; 1.
DR InterPro; IPR005289; GTP-binding_dom.
DR InterPro; IPR006073; GTP1_OBG.
DR InterPro; IPR002917; MMR_HSR1.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PRINTS; PR00326; GTP1_OBG.
DR TIGRFAMS; TIGR00650; MG442; 2.
DR TIGRFAMS; TIGR00231; small_GTP; 2.
KW GTP-binding; Repeat; Complete proteome.
FT NP_BIND 9 16 GTP 1 (POTENTIAL).
FT NP_BIND 56 60 GTP 1 (POTENTIAL).
FT NP_BIND 119 122 GTP 1 (POTENTIAL).
FT NP_BIND 218 225 GTP 2 (POTENTIAL).
FT NP_BIND 265 269 GTP 2 (POTENTIAL).
FT NP_BIND 330 333 GTP 2 (POTENTIAL).
SQ SEQUENCE 483 AA; 53311 MW; 1624111DB29AA266 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 483;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 252 ADWEW 256

RESULT 48
ENG_A BRUSU STANDARD; PRT; 483 AA.
AC Q8G2E8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE GTP-binding protein engA.
GN ENGA OR BR0375.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between

RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CC -!- FUNCTION: GTPase of unknown physiological role.
CC -!- SIMILARITY: Belongs to the era/trmE family of GTP-binding
CC proteins. EngA subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE014349; AAN29321.1; -.
DR TIGR; BR0375; -.
DR HAMAP; MF 00195; -; 1.
DR InterPro; IPR005289; GTP-binding_dom.
DR InterPro; IPR006073; GTP1_OBG.
DR InterPro; IPR002917; MMR_HSR1.
DR InterPro; IPR001806; Ras_trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PRINTS; PR00326; GTP1_OBG.
DR TIGRFAMS; TIGR00650; MG442; 2.
DR TIGRFAMS; TIGR00231; small_GTP; 2.
KW GTP-binding; Repeat; Complete proteome.
FT NP_BIND 9 16 GTP 1 (POTENTIAL).
FT NP_BIND 56 60 GTP 1 (POTENTIAL).
FT NP_BIND 119 122 GTP 1 (POTENTIAL).
FT NP_BIND 218 225 GTP 2 (POTENTIAL).
FT NP_BIND 265 269 GTP 2 (POTENTIAL).
FT NP_BIND 330 333 GTP 2 (POTENTIAL).
SQ SEQUENCE 483 AA; 53281 MW; 776B950CFA036EF3 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 483;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 252 ADWEW 256

RESULT 49
YC42 SYNY3
ID YC42 SYNY3 STANDARD; PRT; 536 AA.
AC P42349;
DT 01-NOV-1995 (Rel. 32, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical methyltransferase all1242 (EC 2.1.1.-) (ORF N).
GN SL1242.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
RN [2]
RP SEQUENCE OF 291-536 FROM N.A.
RX MEDLINE=93222488; PubMed=8467083;
RA Malakhov M.P., Wada H., Los D.A., Sakamoto T., Murata N.;

RT "Structure of a cyanobacterial gene encoding the 50S ribosomal
RT protein L9.";
RL Plant Mol. Biol. 21:913-918(1993).
CC -!- SIMILARITY: TO METHYLTRANSFERASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D90912; BAA18175.1; -;
DR EMBL; D10716; BAA38817.1; -;
DR PIR; S75614; S75614.
DR InterPro; IPR006158; B12-binding.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF02310; B12-binding; 1.
DR Pfam; PF04055; Radical_SAM; 1.
DR SMART; SM00729; Elp3; 1.
KW Hypothetical protein; Transferase; Methyltransferase;
KW Complete proteome.
SQ SEQUENCE 536 AA; 61755 MW; 715F06F2C2D684E3 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 536;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 61 AEWDWA 66

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U39699; AAC71418.1; -;
DR EMBL; U02163; AAD12445.1; -;
DR PIR; A64222; A64222.
DR HSP; P08622; 1BQZ.
DR TIGR; MG200; -;
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DNAJ_1; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
KW Hypothetical protein; Chaperone; Complete proteome.
FT DOMAIN 5 77 J-DOMAIN.
SQ SEQUENCE 601 AA; 68537 MW; F9FAE352E341D093 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 186 DWSW 189

Search completed: July 23, 2004, 13:18:40
Job time : 15 secs

RESULT 50
DNJM_MYCGE
ID DNJM_MYCGE STANDARD; PRT; 601 AA.
AC P47442; Q49288;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DnaJ-like protein MG200.
GN MG200.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 281-409 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:14:39 ; Search time 35 Seconds
(without alignments)
54.089 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	236	3 Q8NJY9	Q8njy9 bionectria
2	37	92.5	274	16 Q8G659	Q8g659 bifidobacte
3	37	92.5	375	5 Q86KS0	Q86ks0 dictyosteli
4	37	92.5	437	16 Q92K30	Q92k30 rhizobium m
5	37	92.5	548	16 Q92M15	Q92mi5 rhizobium m
6	37	92.5	581	5 Q8MSH3	Q8msh3 drosophila
7	37	92.5	597	5 Q9VGP2	Q9vgp2 drosophila
8	37	92.5	610	16 Q86712	Q86712 streptomyce
9	37	92.5	885	16 Q9I389	Q9i389 pseudomonas
10	36	90.0	173	16 Q825E1	Q825e1 streptomyce
11	36	90.0	205	16 Q9ACR5	Q9acr5 streptomyce
12	36	90.0	227	4 Q8IXK8	Q8ixk8 homo sapien
13	36	90.0	228	8 Q7YGU8	Q7ygu8 sphenodon p
14	36	90.0	242	12 Q919K8	Q9i9k8 culex nigri
15	36	90.0	355	11 Q8BIT9	Q8bit9 mus musculu
16	36	90.0	358	10 O50002	O50002 prunus arme

17	36	90.0	374	16 Q9HZ10	Q9hzt10 pseudomonas
18	36	90.0	426	5 Q86KF9	Q86kf9 dictyosteli
19	36	90.0	433	16 Q8P4A1	Q8p4a1 xanthomonas
20	36	90.0	438	16 Q8PFV8	Q8pfv8 xanthomonas
21	36	90.0	452	4 Q96AB7	Q96ab7 homo sapien
22	36	90.0	463	5 Q8MMJ0	Q8mmj0 apis cerana
23	36	90.0	470	12 Q7TF27	Q7tf27 influenza a
24	36	90.0	477	11 Q9CYU6	Q9cyu6 mus musculu
25	36	90.0	484	4 Q9BTV6	Q9btv6 homo sapien
26	36	90.0	605	16 Q82MX2	Q82mx2 streptomyce
27	36	90.0	686	16 Q8FQZ9	Q8fqz9 corynebacte
28	36	90.0	861	16 Q88NQ1	Q88nq1 pseudomonas
29	36	90.0	889	16 Q9AAZ6	Q9aaz6 caulobacter
30	36	90.0	1005	10 Q9XGZ2	Q9xgz2 arabidopsis
31	36	90.0	1324	16 Q820F9	Q820f9 streptomyce
32	36	90.0	5435	2 Q9L4X2	Q9l4x2 streptomyce
33	35	87.5	527	16 Q829Q9	Q829q9 streptomyce
34	34	85.0	166	4 Q8NBW1	Q8nbw1 homo sapien
35	34	85.0	273	10 Q94JM4	Q94jm4 arabidopsis
36	34	85.0	273	10 Q940D6	Q940d6 arabidopsis
37	34	85.0	275	10 Q65710	Q65710 arabidopsis
38	34	85.0	337	11 Q80UX8	Q80ux8 mus musculu
39	34	85.0	376	3 Q9UVL4	Q9uvl4 penicillium
40	34	85.0	617	10 P93050	P93050 arabidopsis
41	34	85.0	1074	16 Q8PJ70	Q8pj70 xanthomonas
42	34	85.0	1842	3 Q96WT6	Q96wt6 schizosacch
43	34	85.0	1842	3 Q96WT7	Q96wt7 schizosacch
44	34	85.0	1842	3 Q96WT8	Q96wt8 schizosacch
45	33	82.5	49	6 Q8SPL6	Q8spl6 equus cabal
46	33	82.5	98	5 Q9VB45	Q9vb45 drosophila
47	33	82.5	136	2 Q8KZ39	Q8kz39 uncultured
48	33	82.5	154	11 Q8BGD2	Q8bgd2 mus musculu
49	33	82.5	155	16 Q821K8	Q821k8 chlamydophi
50	33	82.5	159	10 Q84UN9	Q84un9 oryza sativ

ALIGNMENTS

RESULT 1

Q8NJY9	Q8NJY9	PRELIMINARY;	PRT;	236 AA.
ID	Q8NJY9			
AC	Q8NJY9;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Endoglucanase.			
GN	CEL12C.			
OS	Bionectria ochroleuca (Gliocladium roseum).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.			
OX	NCBI_TaxID=29856;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22067395; PubMed=12073090;			
RA	Goedegebuur F., Fowler T., Phillips J., van der Kley P.,			
RA	van Solingen P., Dankmeyer L., Power S.D.;			
RT	"Cloning and relational analysis of 15 novel fungal endoglucanases			
RT	from family 12 glycosyl hydrolase.";			
RL	Curr. Genet. 41:89-98(2002).			
DR	EMBL; AF435065; AAM77708.1; --			
DR	GO; GO:0008810; F:cellulase activity; IEA.			
DR	GO; GO:0000272; P:polysaccharide catabolism; IEA.			
DR	InterPro; IPR008985; ConA_like lec gl.			
DR	InterPro; IPR002594; Glyco_hydro_12.			
DR	Pfam; PF01670; Glyco_hydro_12; 1.			
DR	ProDom; PD004316; Glyco_hydro_12; 1.			
SQ	SEQUENCE 236 AA; 26024 MW; CJD8A7E33F0C41D8 CRC64;			

Query Match 92.5%; Score 37; DB 3; Length 236;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 63 ADWSWS 68

RESULT 2
Q8G659
ID Q8G659 PRELIMINARY; PRT; 274 AA.
AC Q8G659;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable dihydroorotate dehydrogenase electron transfer subunit.
GN PYRK OR BL0790.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
RA "The genome sequence of Bifidobacterium longum reflects its adaptation
to the human gastrointestinal tract.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
RL EMBL; AE014701; AAN24605.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008333; FAD_binding_6.
DR Pfam; PF00970; FAD_binding_6; 1.
KW Complete proteome.
SQ SEQUENCE 274 AA; 29978 MW; 971E0016E79636DB CRC64;

Query Match 92.5%; Score 37; DB 16; Length 274;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 171 ADWSWS 176

RESULT 3
Q86KS0
ID Q86KS0 PRELIMINARY; PRT; 375 AA.
AC Q86KS0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115612; AAO50929.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR000581; ILVD_EDD_family.
DR InterPro; IPR006970; PT.
DR Pfam; PF04886; PT; 1.
DR PROSITE; PS00886; ILVD_EDD_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 375 AA; 41862 MW; EC9A1D744C56856E CRC64;

Query Match 92.5%; Score 37; DB 5; Length 375;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
: | | | | |
Db 46 SDWSWA 51

RESULT 4
Q92K30
ID Q92K30 PRELIMINARY; PRT; 437 AA.
AC Q92K30;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein R02283.
GN R02283 OR SMC01671.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RA "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
RL EMBL; AL591790; CAC46862.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 437 AA; 48372 MW; 950E0B3DA963CE78 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 437;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 157 ADWNWA 162

RESULT 5
Q92MI5
ID Q92MI5 PRELIMINARY; PRT; 548 AA.
AC Q92MI5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative fatty-acid-CoA ligase protein (EC 6.-.-.-).
GN R02631 OR SMC00741.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591791; CAC47210.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF0501; AMP-binding; 1.
DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 235 ADAWA 240

RESULT 6
Q8MSH3 Q8MSH3 PRELIMINARY; PRT; 581 AA.
AC Q8MSH3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GH24640p.
GN NINAG OR CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118818; AAM50678.1; -.
DR FlyBase; FBgn0037896; ninaG.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000172; GMC_oxred.
DR InterPro; IPR007867; GMC_oxred C.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF05199; GMC_oxred C; 1.
DR Pfam; PF00732; GMC_oxred N; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
SQ SEQUENCE 581 AA; 63475 MW; A2F13BEBBC25E496D CRC64;

Query Match 92.5%; Score 37; DB 5; Length 581;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6

Db 158 SDWSWA 163
:|||||
RESULT 7
Q9VGP2 Q9VGP2 PRELIMINARY; PRT; 597 AA.
ID Q9VGP2;
AC Q9VGP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG6728 protein.
GN NINAG OR CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003691; AAF54634.1; -.
DR FlyBase; FBgn0037896; ninaG.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000172; GMC_oxred.
DR InterPro; IPR007867; GMC_oxred C.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF05199; GMC_oxred C; 1.
DR Pfam; PF00732; GMC_oxred N; 1.
DR PROSITE; PS00624; GMC_OXRED_2; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.

SQ	SEQUENCE	597 AA; 65274 MW; 8C4C362AFFA0902A CRC64;			
	Query Match	92.5%; Score 37; DB 5; Length 597;			
	Best Local Similarity	83.3%; Pred. No. 5.7e+02;			
	Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1 ADWSWA 6				
Db	158 SDWSWA 163				
RESULT 8					
O86712					
ID	O86712	PRELIMINARY; PRT; 610 AA.			
AC	O86712;				
DT	01-NOV-1998 (TrEMBLrel. 08, Created)				
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Hypothetical protein SC06530.				
GN	SCO6530 OR SC5C7.15.				
OS	Streptomyces coelicolor.				
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
OC	Streptomycineae; Streptomycetaceae; Streptomyces.				
OX	NCBI_TaxID=1902;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=A3(2) / M145;				
RX	MEDLINE=21996410; PubMed=12000953;				
RA	Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,				
RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,				
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,				
RA	Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,				
RA	Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,				
RA	Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,				
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,				
RA	Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,				
RA	Hopwood D.A.;				
RT	"Complete genome sequence of the model actinomycete Streptomyces				
RT	coelicolor A3(2).";				
RL	Nature 417:141-147(2002).				
DR	EMBL; AL939128; CAA20627.1; --				
DR	PIR; T35222; T35222.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 610 AA; 67368 MW; 052CEA90DB589021 CRC64;				
	Query Match	92.5%; Score 37; DB 16; Length 610;			
	Best Local Similarity	83.3%; Pred. No. 5.9e+02;			
	Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1 ADWSWA 6				
Db	83 ADAWA 88				
RESULT 9					
Q9I389					
ID	Q9I389	PRELIMINARY; PRT; 885 AA.			
AC	Q9I389;				
DT	01-MAR-2001 (TrEMBLrel. 16, Created)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Two-component sensor KdpD.				
GN	KDPD OR PA1636.				
OS	Pseudomonas aeruginosa.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;				
OC	Pseudomonadaceae; Pseudomonas.				
OX	NCBI_TaxID=287;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 15692 / PAO1;				
RX	MEDLINE=20437337; PubMed=10984043;				
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,				
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,				

RA	Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,				
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,				
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,				
RA	Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;				
RT	"Complete genome sequence of Pseudomonas aeruginosa PAO1, an				
RT	opportunistic pathogen.";				
RL	Nature 406:959-964(2000).				
CC	-I- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.				
DR	EMBL; AE004591; AAG05025.1; --				
DR	PIR; C83441; C83441.				
DR	HSSP; P02933; LJOY.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0005524; F:ATP binding; IEA.				
DR	GO; GO:0016301; F:kinase activity; IEA.				
DR	GO; GO:0016740; F:transferase activity; IEA.				
DR	GO; GO:0000155; F:two-component sensor molecule activity; IEA.				
DR	GO; GO:0006950; P:response to stress; IEA.				
DR	GO; GO:0007600; P:sensory perception; IEA.				
DR	GO; GO:0007165; P:signal transduction; IEA.				
DR	InterPro; IPR003594; ATPbind ATPase.				
DR	InterPro; IPR004358; Bact_sens_pr_C.				
DR	InterPro; IPR003018; GAF.				
DR	InterPro; IPR005467; His_kinase.				
DR	InterPro; IPR003661; His_kinA_N.				
DR	InterPro; IPR003852; KdpD.				
DR	InterPro; IPR006016; Usp_dom.				
DR	Pfam; PF02518; HATPase_c; 1.				
DR	Pfam; PF00512; Hiska; 1.				
DR	Pfam; PF02702; KdpD; 1.				
DR	Pfam; PF00582; Usp; 1.				
DR	PRINTS; PR00344; BCTRLSENSOR.				
DR	ProDom; PD011725; KdpD; 1.				
DR	SMART; SM00065; GAF; 1.				
DR	SMART; SM00387; HATPase_c; 1.				
DR	SMART; SM00388; Hiska; 1.				
DR	PROSITE; PS0109; HIS_KIN; 1.				
KW	Kinase; Phosphorylation; Sensory transduction; Transferase;				
KW	Complete proteome.				
SQ	SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;				
	Query Match	92.5%; Score 37; DB 16; Length 885;			
	Best Local Similarity	83.3%; Pred. No. 8.5e+02;			
	Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1 ADWSWA 6				
Db	563 ADAWA 568				
RESULT 10					
Q825E1					
ID	Q825E1	PRELIMINARY; PRT; 173 AA.			
AC	Q825E1;				
DT	01-JUN-2003 (TrEMBLrel. 24, Created)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Hypothetical protein.				
GN	SAV7517.				
OS	Streptomyces avermitilis.				
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
OC	Streptomycineae; Streptomycetaceae; Streptomyces.				
OX	NCBI_TaxID=33903;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;				
RX	MEDLINE=21477403; PubMed=11572948;				
RA	Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,				
RA	Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,				
RA	Kikuchi H., Shiba T., Sakaki Y., Hattori M.;				
RT	"Genome sequence of an industrial microorganism Streptomyces				
RT	avermitilis: deducing the ability of producing secondary				
RT	metabolites.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).				


```
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP05050; BAC75228.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 173 AA; 18912 MW; 22B26C7D2222CA60 CRC64;

Query Match          90.0%; Score 36; DB 16; Length 173;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db |||||
53 ADWEWA 58

RESULT 11
Q9ACRS5
ID Q9ACRS5 PRELIMINARY; PRT; 205 AA.
AC Q9ACRS5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCPI.253.
GN SCPI.253.
OS Streptomyces coelicolor.
OG Plasmid SCPI.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Lark L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL590464; CAC36779.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 205 AA; 23051 MW; 6602396CFF93F2D9 CRC64;

Query Match          90.0%; Score 36; DB 16; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db |||||
10 ADWSW 14

RESULT 12
Q8IXK8
ID Q8IXK8 PRELIMINARY; PRT; 227 AA.
AC Q8IXK8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
```

```
DE Similar to hypothetical protein BC017335.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040173; AAH40173.1; -.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25487 MW; F11A71BA57062A05 CRC64;

Query Match          90.0%; Score 36; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db |||||
113 ADWSW 117

RESULT 13
Q7YGU8
ID Q7YGU8 PRELIMINARY; PRT; 228 AA.
AC Q7YGU8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit II.
OS Sphenodon punctatus (Hatteria) (Tuatara).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
OX NCBI_TaxID=8508;
RN [1]
RP SEQUENCE FROM N.A.
RA Rest J.S., Ast J.C., Austin C.C., Waddell P.J., Tibbetts E.A.,
RA Hay J.M., Mindell D.P.;
RT "Molecular systematics of primary reptilian lineages and the tuatara
RT mitochondrial genome.";
RL Mol. Phylogenet. Evol. 0:0-0(2003).
DR EMBL; AF534390; AAP42708.1; -.
KW Mitochondrion.
SQ SEQUENCE 228 AA; 25903 MW; AC52448F76C9F0A4 CRC64;

Query Match          90.0%; Score 36; DB 8; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db |||||
221 DWSWA 225

RESULT 14
Q919K8
ID Q919K8 PRELIMINARY; PRT; 242 AA.
AC Q919K8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CUN068 hypothetical protein.
GN CUN068.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_TaxID=130556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RX MEDLINE=21488685; PubMed=11602755;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
```



```
RA Becnel J.J., Rock D.L., Kutish G.F.;;
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";
RL J. Virol. 75:11157-11165(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF403738; AAK94146.1; -.
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match          90.0%; Score 36; DB 12; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 80 DWSWA 84

RESULT 15
Q8BIT9
ID Q8BIT9 PRELIMINARY; PRT; 355 AA.
AC Q8BIT9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
GN 2810443J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK087998; BAC40084.1; -.
DR MGD; MGI:1914478; 2810443J12Rik.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
SQ SEQUENCE 355 AA; 40183 MW; FEF8546127402D58 CRC64;

Query Match          90.0%; Score 36; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 215 ADWSW 219

RESULT 16
O50002
ID O50002 PRELIMINARY; PRT; 358 AA.
AC O50002;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cysteine protease.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
```

```
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bergeron; TISSUE=Mesocarp, and Exocarp;
RA Mbeguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;
RT "Sequence of AFTP1, a Cysteine Proteinase From Apricot Fruit
RT (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
RT 179).";
RL Plant Physiol. 115:1730-1730(1997).
DR EMBL; U93166; AAB97142.1; -.
DR HSSP; P07711; 1CJL.
DR MEROPS; C01.041; -.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00640; THIOI_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;

Query Match          90.0%; Score 36; DB 10; Length 358;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 108 ADWSW 112

RESULT 17
Q9HZ10
ID Q9HZ10 PRELIMINARY; PRT; 374 AA.
AC Q9HZ10;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004746; AAG06618.1; -.
DR PIR; B83241; B83241.
DR InterPro; IPR007434; DUF482.
DR Pfam; PF04339; DUF482; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match          90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
```


DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF0324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 183 DWSWA 187

RESULT 21
Q96AB7 PRELIMINARY; PRT; 452 AA.
AC Q96AB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017335; AAH17335.1; -.
DR EMBL; AK075115; BAC11411.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25EE38096733 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 338 ADWSW 342

RESULT 22
Q8MMJ0 PRELIMINARY; PRT; 463 AA.
ID Q8MMJ0
AC Q8MMJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Major royal jelly protein MRJP2 precursor.

GN MRJP2.
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nurse heads;
RA Sittipraneed S., Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis cerana in Thailand.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525777; AAM88282.1; -.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal.
FT SIGNAL 1 17 POTENTIAL.
SQ SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;

Query Match 90.0%; Score 36; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 110 DWSWA 114

RESULT 23
Q7TF27 PRELIMINARY; PRT; 470 AA.
ID Q7TF27
AC Q7TF27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neuraminidase.
OS Influenza A virus (A/duck/NY/191255-59/02(H5N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=232442;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/duck/NY/191255-59/02;
RA Lee C.-W., Senne D., Linares J.A., Woolcock P., Stallnecht D.,
RA Spackman E., Swayne D., Suarez D.;
RT "Characterization of recent H5 subtype avian influenza viruses from U.S. poultry.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY300948; AAP57560.1; -.
SQ SEQUENCE 470 AA; 52260 MW; 41470434D8ED1662 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 470;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 24
Q9CYU6 PRELIMINARY; PRT; 477 AA.
ID Q9CYU6
AC Q9CYU6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2810443J12Rik protein (Mitochondrial ribosomal protein L41 homolog).
GN 2810443J12RIK.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK013297; BAB28775.1; -.
DR EMBL; AK078448; BAC37279.1; -.
DR MGD; MGI:1914478; 2810443J12Rik.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 477 AA; 53201 MW; 2655573524A4BA9C CRC64;

Query Match 90.0%; Score 36; DB 11; Length 477;
Best Local Similarity 100.0%; Pred.No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 337 ADWSW 341

RESULT 25
Q9BTV6
ID Q9BTV6 PRELIMINARY; PRT; 484 AA.
AC Q9BTV6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003123; AAH03123.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT NON TER 1
SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7358E CRC64;

Query Match 90.0%; Score 36; DB 4; Length 484;
Best Local Similarity 100.0%; Pred.No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 370 ADWSW 374

RESULT 26
Q82MX2
ID Q82MX2 PRELIMINARY; PRT; 605 AA.
AC Q82MX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative nitric oxide synthase.
GN SAV1531.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005027; BAC69241.1; -.
DR GO; GO:0004517; F: nitric-oxide synthase activity; IEA.
DR GO; GO:0006809; P: nitric oxide biosynthesis; IEA.
DR InterPro; IPR004030; NO_synthase.
DR Pfam; PF02898; NO_synthase; 1.
DR PROSITE; PS60001; NOS; 1.
KW Complete proteome.
SQ SEQUENCE 605 AA; 65534 MW; 8208F93B381C1FF5 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 605;
Best Local Similarity 100.0%; Pred.No. 8.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 556 ADWSW 560

RESULT 27


```
Q8FQZ9
ID Q8FQZ9 PRELIMINARY; PRT; 686 AA.
AC Q8FQZ9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ATP-dependent DNA helicase.
GN CE0968.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005217; BAC17778.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006259; P:DNA metabolism; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_box.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR004589; RecQ.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICc; 1.
DR TIGRFAMS; TIGR00614; recQ_fam; 1.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
KW Helicase; Complete proteome.
SQ SEQUENCE 686 AA; 74505 MW; 6AAD7AA52B892A27 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 686;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 567 ADWDWA 572

RESULT 28
Q88NQ1 PRELIMINARY; PRT; 861 AA.
AC Q88NQ1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sensory box protein.
GN PP1154.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzappple E., Scanlan D., Tran K., Moazzez A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
```

```
metabolically versatile Pseudomonas putida KT2440.";
RT Environ. Microbiol. 4:799-808(2002).
RL EMBL; AE016778; AAN66779.1; -.
DR TIGR; PP1154; -.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR007892; CHASE4.
DR InterPro; IPR001633; EAL.
DR InterPro; IPR000160; GGDEF.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS domain.
DR InterPro; IPR000437; ProK_lipoprot_s.
DR Pfam; PF05228; CHASE4; 1.
DR Pfam; PF00563; EAL; 1.
DR Pfam; PF00990; GGDEF; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PROSITE; PS50883; EAL; 1.
DR PROSITE; PS50887; GGDEF; 1.
DR PROSITE; PS50112; PAS; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 861 AA; 95980 MW; 64D652AFC7C3B9D6 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 861;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 91 ADWQWA 96

RESULT 29
Q9AAZ6 PRELIMINARY; PRT; 889 AA.
AC Q9AAZ6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TonB-dependent receptor.
GN CC0446.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005717; AAK22433.1; -.
DR PIR; E87304; E87304.
DR TIGR; CC0446; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00593; TonB_dep_Rec; 1.
KW Receptor; Complete proteome.
SQ SEQUENCE 889 AA; 95775 MW; 75FCBD7A726A01A5 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 889;
```


Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 0;

QY 1 ADWSW 5
Db 618 ADWSW 622

RESULT 30

Q9XGZ2 Q9XGZ2 PRELIMINARY; PRT; 1005 AA.
AC Q9XGZ2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T1N24.22 protein (Putative receptor protein kinase).
GN T1N24.22 OR AT5G25930.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Washu;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Murray J., Langston Y., Clarke K., Drone K.;
RT "The sequence of A. thaliana T1N24.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Waterston R.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF149413; AAD40144.1; -.
DR EMBL; BT004058; AAO42089.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 1005 AA; 111963 MW; BB006438CC9541C9 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 0;

QY 1 ADWSW 5
Db 906 ADWSW 910

RESULT 31

Q820F9 Q820F9 PRELIMINARY; PRT; 1324 AA.
AC Q820F9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative FtsK/spoIIIE family protein.
GN SAV5442.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005042; BAC73154.1; -.
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR InterPro; IPR000834; Peptidase_M14.
DR Pfam; PF01580; FtsK_SpoIIIE; 2.
DR SMART; SM00382; AAA; 3.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
DR PROSITE; PS50901; FTSK_SPOIIIE; 3.
KW Complete proteome.
SQ SEQUENCE 1324 AA; 143398 MW; 8E24138D58089456 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 1324;
Best Local Similarity 83.3%; Pred. No. 1.8e+03; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 254 ADWEWA 259

RESULT 32

Q9L4X2 Q9L4X2 PRELIMINARY; PRT; 5435 AA.
AC Q9L4X2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NysJ.
SQ SEQUENCE 1005 AA; 111963 MW; BB006438CC9541C9 CRC64;

GN NYSJ.
OS Streptomyces noursei.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1971;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 11455;
RX MEDLINE=20334850; PubMed=10873841;
RA Brautaset T., Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.R.,
RA Valla S., Zotchev S.B.;
RT "Biosynthesis of the polyene antifungal antibiotic nystatin in
RT Streptomyces noursei ATCC 11455: analysis of the gene cluster and
RT deduction of the biosynthetic pathway.";
RL Chem. Biol. 7:395-403(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL; AF263912; AAF71767.1; -.
DR HSSP; P25715; 1MLA.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0004314; F:[acyl-carrier protein] S-malonyltransferase. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac trans.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR004410; FabD.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR006162; Ppantne_S.
DR InterPro; IPR006163; Pp_bind.
DR Pfam; PF00698; Acyl_transf; 3.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF00109; ketoacyl-synt; 3.
DR Pfam; PF02801; ketoacyl-synt_C; 3.
DR Pfam; PF00550; pp-binding; 3.
DR TIGRFAMS; TIGR00128; fabD; 3.
DR PROSITE; PS50075; ACP_DOMAIN; 3.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 3.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
KW Oxidoreductase; Phosphopantetheine; Transferase.
SQ SEQUENCE 5435 AA; 562659 MW; AA55465DF087A38C CRC64;

Query Match 90.0%; Score 36; DB 2; Length 5435;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 1525 ADWSW 1529

RESULT 33
Q829Q9 ID Q829Q9 PRELIMINARY; PRT; 527 AA.
AC Q829Q9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN SAV6350.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005046; BAC74061.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 527 AA; 57663 MW; B8E5D28F9CD77148 CRC64;

Query Match 87.5%; Score 35; DB 16; Length 527;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 521 ADWPWA 526

RESULT 34
Q8NBW1 ID Q8NBW1 PRELIMINARY; PRT; 166 AA.
AC Q8NBW1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90714.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK075195; BAC11463.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR000379; Ser_estrs.
KW Hypothetical protein.
SQ SEQUENCE 166 AA; 18985 MW; 1C23AB4254636618 CRC64;

Query Match 85.0%; Score 34; DB 4; Length 166;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 19 ASWSWA 24

RESULT 35
Q94JM4 ID Q94JM4 PRELIMINARY; PRT; 273 AA.
AC Q94JM4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AT4g19390/T5K18_170.

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378856; AAK55659.1; -.
SQ SEQUENCE 273 AA; 30043 MW; B0CABDBE88971B3A CRC64;

Query Match 85.0%; Score 34; DB 10; Length 273;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 57 SDWSWS 62

RESULT 36
Q940D6
ID Q940D6 PRELIMINARY; PRT; 273 AA.
AC Q940D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AT4g19390/T5K18.170.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055785; AAL06952.1; -.
SQ SEQUENCE 273 AA; 30085 MW; 518FA9EFD9D2003B CRC64;

Query Match 85.0%; Score 34; DB 10; Length 273;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 57 SDWSWS 62

RESULT 37
O65710
ID O65710 PRELIMINARY; PRT; 275 AA.
AC O65710;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.

GN T5K18.170 OR AT4Gi9390.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Van Der Schueren J., Chuang Y.-J., Voet M., Robben J., C.;
RA Volckaert G., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Van Der Schueren J., Chuang Y.J., Aert R., Defoor E., Robben J.,
RA Volckaert G., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022580; CAA18626.1; -.
DR EMBL; AL161550; CAB78941.1; -.
DR PIR; T05822; T05822.
KW Hypothetical protein.
SQ SEQUENCE 275 AA; 30289 MW; 5157A10663950B62 CRC64;

Query Match 85.0%; Score 34; DB 10; Length 275;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 57 SDWSWS 62

RESULT 38
Q80UX8
ID Q80UX8 PRELIMINARY; PRT; 337 AA.
AC Q80UX8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE I110065L07Rik protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.


```
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043690; AAH43690.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR000379; Ser_estrs.
SQ SEQUENCE 337 AA; 38525 MW; 0EAA241B44567B09 CRC64;

Query Match      85.0%; Score 34; DB 11; Length 337;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      19 ASWSWA 24

RESULT 39
Q9UVL4
ID Q9UVL4 PRELIMINARY; PRT; 376 AA.
AC Q9UVL4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyalacturonase (EC 3.2.1.15).
GN PGGI.
OS Penicillium griseoroseum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eubotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=84562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCT 6421;
RA Ribon A.O.B., D'Angelo M.A.C., Coelho J.L.C., Queiroz M.V.,
RA Araujo E.F.;
RT "Differential expression of polygalacturonases genes from Penicillium
RT griseoroseum.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
CC (POLYGALACTURONASES).
DR EMBL; AF195791; AAF06810.1; -.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0004650; F:polygalacturonase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006626; PbH1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SMO0710; PbH1; 5.
DR PROSITE; PS00502; POLYGALACTURONASE; 1.
KW Cell wall; Glycosidase; Hydrolase.
SQ SEQUENCE 376 AA; 38038 MW; 03707373B5B8C258 CRC64;

Query Match      85.0%; Score 34; DB 3; Length 376;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      349 SDWSWS 354

RESULT 40
P93050
ID P93050 PRELIMINARY; PRT; 617 AA.
AC P93050;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATPK2324 (AT2G48010/T9J23.16).
GN RKF3 OR T9J23.16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

```
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA C24;
RA Kertbundit S., Linacero R., Rouze P., Galis I., Macas J., Deboeck F.,
RA Hernalsteens J., De Greve H.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Takahashi T., Mu J.-H., Gasch A., Chua N.-H.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
RA Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z84202; CAB06335.1; -.
DR EMBL; AF024650; AAC50045.1; -.
DR EMBL; AC006072; AAD13705.1; -.
DR EMBL; AY037237; AAK59837.1; -.
DR EMBL; BT000518; AAN18087.1; -.
DR FIR; C84922; C84922.
DR HSSP; P12931; 1FMK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000504; RNA_rec_mot.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
```


DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR004568; Pantethn_trn.
DR InterPro; IPR006162; Ppantne_S.
DR Pfam; PF01648; ACPS; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
KW Transferase.
SQ SEQUENCE 1842 AA; 202138 MW; B8BF4D29C29E383B CRC64;

Query Match 85.0%; Score 34; DB 3; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 400 SDWNWA 405

RESULT 44
Q96WT8 PRELIMINARY; PRT; 1842 AA.
AC Q96WT8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fatty acid synthase alpha-subunit.
GN FAS2.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=fas2/lsl1-H201;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fatty acid synthase temperature-sensitive mutant strains of the
RT fission yeast Schizosaccharomyces pombe fas2/lsl1.";
RL Biochim. Biophys. Acta 1532:223-233(2001).
DR EMBL; AB013748; BAB62030.1; -.
DR PIR; A54083; A54083.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR004568; Pantethn_trn.
DR InterPro; IPR006162; Ppantne_S.
DR Pfam; PF01648; ACPS; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMS; TIGR00556; pantethn_trn; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
KW Transferase.
SQ SEQUENCE 1842 AA; 202156 MW; F2F9612BEE3EE316 CRC64;

Query Match 85.0%; Score 34; DB 3; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 400 SDWNWA 405

RESULT 45
Q8SPL6 PRELIMINARY; PRT; 49 AA.
AC Q8SPL6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endothelia NO synthase (Fragment).
GN ENOS.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RA Welter H., Bollwein H., Einspanier R.;
RT "Expression of horse endometrium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439886; CAD29177.1; -.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IEA.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IEA.
DR InterPro; IPR004030; NO_synthase.
DR Pfam; PF02898; NO_synthase; 1.
DR NON_TER 1
FT NON_TER 49
FT NON_TER 49
SQ SEQUENCE 49 AA; 5566 MW; 82B3B2247F820E63 CRC64;

Query Match 82.5%; Score 33; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 15 ADWAW 19

RESULT 46
Q9VB45 PRELIMINARY; PRT; 98 AA.
AC Q9VB45;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG3348 protein.
GN CG3348.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:
Db 90 ADWNW 94

RESULT 50
Q84UN9
ID Q84UN9 PRELIMINARY; PRT; 159 AA.
AC Q84UN9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE B1027A11.9 protein.
GN B1027A11.9.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
RT clone:B1027A11.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005464; BAC66742.1; -.
SQ SEQUENCE 159 AA; 16692 MW; B3B044A8EA1C4427 CRC64;

Query Match 82.5%; Score 33; DB 10; Length 159;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||:
Db 80 DWAWA 84

Search completed: July 23, 2004, 13:19:28
Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:19:59 ; Search time 35 Seconds
(without alignments)
54.089 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 6
Sequence: 1 ADWSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 1017041 seqs, 315518202 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

- Database : SPTREMBL 25.*
- 1: sp_archea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_virus.*
 - 16: sp_bacteriap.*
 - 17: sp_archheap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	83.3	205	16	Q9ACR5 streptomyce
2	5	83.3	227	4	Q8IXK8 homo sapien
3	5	83.3	228	8	Q7YGU8 sphenodon p
4	5	83.3	236	3	Q8NJY9 bionectria
5	5	83.3	242	12	Q919K8 culex nigri
6	5	83.3	274	16	Q8G659 bifidobacte
7	5	83.3	355	11	Q8BIT9 mus musculu
8	5	83.3	358	10	Q50002 prunus arme
9	5	83.3	374	16	Q9HZ10 pseudomonas
10	5	83.3	375	5	Q86KS0 dictyosteli
11	5	83.3	426	5	Q86KF9 dictyosteli
12	5	83.3	433	16	Q8P4A1 xanthomonas
13	5	83.3	438	16	Q8PFV8 xanthomonas
14	5	83.3	452	4	Q96AB7 homo sapien
15	5	83.3	463	5	Q8MMJ0 apis cerana
16	5	83.3	470	12	Q7TF27 influenza a

90	4	66.7	151	16	Q9JTTQ4	Q9jttq4 neisseria m	163	4	66.7	208	16	Q8REU4	Q8reu4 fusobacteri
91	4	66.7	152	15	Q9J6E9	Q9j6e9 human immun	164	4	66.7	210	2	Q84BA4	Q84ba4 erwinia chr
92	4	66.7	152	16	Q8YJJC8	Q8yjc8 brucella me	165	4	66.7	210	5	Q9XUL5	Q9xul5 caenorhabdi
93	4	66.7	152	16	Q8FYH0	Q8fyh0 brucella su	166	4	66.7	210	16	Q9A684	Q9a684 caulobacter
94	4	66.7	153	17	O58545	O58545 pyrococcus	167	4	66.7	211	9	O80148	O80148 bacterioph
95	4	66.7	154	10	O8L4J1	O8l4j1 cucumis mel	168	4	66.7	211	9	O21903	O21903 bacterioph
96	4	66.7	154	10	O8LK69	O8lk69 cucumis sat	169	4	66.7	212	16	Q89WM0	Q89wm0 bradyrhizob
97	4	66.7	154	10	O8LK96	O8lk96 cucumis mel	170	4	66.7	213	13	Q801Y7	Q801y7 brachydanio
98	4	66.7	154	10	O8LK70	O8lk70 cucumis sat	171	4	66.7	213	16	Q82HK2	Q82hk2 streptomyce
99	4	66.7	154	16	O81GT0	O81gt0 bacillus ce	172	4	66.7	214	16	Q9KFX7	Q9kfx7 bacillus ha
100	4	66.7	155	10	O8L5A9	O8l5a9 cucumis sat	173	4	66.7	214	16	Q82K45	Q82k45 salmonella
101	4	66.7	155	11	Q7TSQ4	Q7tsq4 arvicanthis	174	4	66.7	214	16	Q8Z143	Q8z143 salmonella
102	4	66.7	156	16	Q7U3L6	Q7u3l6 synechococc	175	4	66.7	215	4	Q9H6Z2	Q9h6z2 homo sapien
103	4	66.7	160	16	Q88NT5	Q88nt5 pseudomonas	176	4	66.7	215	11	Q8VDR5	Q8vdr5 mus musculu
104	4	66.7	161	16	Q8U535	Q8u535 agrobacteri	177	4	66.7	215	11	Q8BTD1	Q8btd1 mus musculu
105	4	66.7	161	16	Q8A6Y5	Q8a6y5 bacteroides	178	4	66.7	216	2	Q8GEU0	Q8geu0 gamma-prote
106	4	66.7	163	10	O82086	O82086 zea mays (m	179	4	66.7	216	5	Q8SSZ2	Q8ssz2 sarcophaga
107	4	66.7	164	11	Q9EP94	Q9ep94 mus musculu	180	4	66.7	216	16	Q7WJG3	Q7wjg3 bordetella
108	4	66.7	165	11	Q9CY62	Q9cy62 mus musculu	181	4	66.7	216	16	Q7WAC2	Q7wac2 bordetella
109	4	66.7	166	4	Q8NBW1	Q8nbw1 homo sapien	182	4	66.7	217	2	O52796	O52796 amycolatops
110	4	66.7	166	16	Q8Z5E0	Q8z5e0 salmonella	183	4	66.7	218	15	P90011	P90011 human immun
111	4	66.7	166	16	Q7WGY9	Q7wgy9 bordetella	184	4	66.7	218	15	P90005	P90005 human immun
112	4	66.7	166	16	Q7W9R9	Q7w9r9 bordetella	185	4	66.7	218	15	P90005	P90005 human immun
113	4	66.7	166	16	Q7VWA7	Q7vwa7 bordetella	186	4	66.7	218	15	P90019	P90019 human immun
114	4	66.7	168	4	Q96NQ0	Q96ng0 homo sapien	187	4	66.7	218	15	P90026	P90026 human immun
115	4	66.7	168	16	Q98K83	Q98k83 rhizobium l	188	4	66.7	218	15	P88066	P88066 human immun
116	4	66.7	169	5	Q9VKF4	Q9vkf4 drosophila	189	4	66.7	218	15	P88071	P88071 human immun
117	4	66.7	171	2	Q9FAY5	Q9fay5 pseudomonas	190	4	66.7	218	15	P90008	P90008 human immun
118	4	66.7	172	10	O8LJQ4	O8ljq4 prunus pers	191	4	66.7	218	15	P90020	P90020 human immun
119	4	66.7	175	5	Q9VBB9	Q9vbb9 drosophila	192	4	66.7	218	15	P88075	P88075 human immun
120	4	66.7	178	10	Q8LHJ6	Q8lhj6 oryza sativ	193	4	66.7	218	15	P88077	P88077 human immun
121	4	66.7	178	16	Q9HT17	Q9ht17 pseudomonas	194	4	66.7	218	15	P89999	P89999 human immun
122	4	66.7	180	16	Q9HZB0	Q9hzb0 pseudomonas	195	4	66.7	218	15	P90023	P90023 human immun
123	4	66.7	180	16	Q984C9	Q984c9 rhizobium l	196	4	66.7	218	15	P89970	P89970 human immun
124	4	66.7	180	16	Q8PJ85	Q8pj85 xanthomonas	197	4	66.7	218	15	P90001	P90001 human immun
125	4	66.7	181	16	O8EJ28	O8ej28 shewanella	198	4	66.7	218	15	P90003	P90003 human immun
126	4	66.7	181	16	Q82FZ7	Q82fz7 streptomyce	199	4	66.7	218	15	P90009	P90009 human immun
127	4	66.7	182	16	Q8P6I6	Q8p6i6 xanthomonas	200	4	66.7	218	15	P90015	P90015 human immun
128	4	66.7	185	16	Q88LD6	Q88ld6 pseudomonas	201	4	66.7	218	15	P90018	P90018 human immun
129	4	66.7	188	16	Q9CKZ8	Q9ckz8 pasteurella	202	4	66.7	218	15	P90002	P90002 human immun
130	4	66.7	188	16	Q92V87	Q92v87 rhizobium m	203	4	66.7	218	15	P88072	P88072 human immun
131	4	66.7	189	2	Q849H0	Q849h0 streptomyce	204	4	66.7	218	15	P90010	P90010 human immun
132	4	66.7	189	16	Q89VR9	Q89vr9 bradyrhizob	205	4	66.7	218	15	P90012	P90012 human immun
133	4	66.7	189	16	Q7WR37	Q7wr37 bordetella	206	4	66.7	218	15	P88070	P88070 human immun
134	4	66.7	189	16	Q7W271	Q7w271 bordetella	207	4	66.7	218	15	P88073	P88073 human immun
135	4	66.7	190	16	Q8Z7X5	Q8z7x5 salmonella	208	4	66.7	218	15	P90014	P90014 human immun
136	4	66.7	191	16	Q8PNV6	Q8pnv6 xanthomonas	209	4	66.7	218	15	P90025	P90025 human immun
137	4	66.7	191	17	O29160	O29160 archaeoglob	210	4	66.7	218	15	P90024	P90024 human immun
138	4	66.7	192	6	Q9BGX8	Q9bgx8 macaca fasc	211	4	66.7	218	15	P90022	P90022 human immun
139	4	66.7	192	10	Q7XVE3	Q7xve3 oryza sativ	212	4	66.7	218	15	P90000	P90000 human immun
140	4	66.7	193	16	Q835M7	Q835m7 enterococcu	213	4	66.7	218	15	P90021	P90021 human immun
141	4	66.7	194	11	Q9EPC4	Q9epc4 mus musculu	214	4	66.7	218	15	P89998	P89998 human immun
142	4	66.7	194	16	Q9A7S1	Q9a7s1 caulobacter	215	4	66.7	218	15	P90013	P90013 human immun
143	4	66.7	195	4	Q96LW6	Q96lw6 homo sapien	216	4	66.7	218	15	P88074	P88074 human immun
144	4	66.7	195	16	Q87YI5	Q87yi5 pseudomonas	217	4	66.7	218	15	P90004	P90004 human immun
145	4	66.7	196	16	Q9A6I2	Q9a6i2 caulobacter	218	4	66.7	218	15	P88076	P88076 human immun
146	4	66.7	200	16	O54163	O54163 streptomyce	219	4	66.7	218	15	P90006	P90006 human immun
147	4	66.7	200	16	Q88XZ4	Q88xz4 lactobacill	220	4	66.7	218	15	P90016	P90016 human immun
148	4	66.7	201	16	Q82NK5	Q82nk5 streptomyce	221	4	66.7	218	15	P90007	P90007 human immun
149	4	66.7	203	2	Q9WWG7	Q9wwg7 pseudomonas	222	4	66.7	218	15	P88069	P88069 human immun
150	4	66.7	203	16	O51366	O51366 borrelia bu	223	4	66.7	218	15	P88068	P88068 human immun
151	4	66.7	203	16	O51367	O51367 borrelia bu	224	4	66.7	218	16	Q8XT57	Q8xt57 ralstonia s
152	4	66.7	204	16	Q7VZD0	Q7vzd0 bordetella	225	4	66.7	218	16	Q7UJW3	Q7ujw3 rhodopirell
153	4	66.7	205	5	Q7YVW0	Q7yvw0 caenorhabdi	226	4	66.7	219	16	Q8EZY2	Q8ezy2 leptospira
154	4	66.7	205	16	Q69756	Q69756 pseudomonas	227	4	66.7	223	4	Q8WYI3	Q8wyi3 homo sapien
155	4	66.7	206	16	Q9PBA5	Q9pba5 xylella fas	228	4	66.7	223	5	Q9NDX8	Q9ndx8 theileria s
156	4	66.7	206	16	Q9HV17	Q9hv17 pseudomonas	229	4	66.7	223	5	Q9XXX1	Q9xxx1 theileria b
157	4	66.7	206	16	Q8RTK1	Q8rtk1 xanthomonas	230	4	66.7	223	5	Q26545	Q26545 schistosoma
158	4	66.7	206	16	Q8PMV6	Q8pmv6 xanthomonas	231	4	66.7	223	5	Q9NDX7	Q9ndx7 theileria s
159	4	66.7	206	16	Q87C12	Q87c12 xylella fas	232	4	66.7	223	16	Q81XU7	Q81xu7 bacillus an
160	4	66.7	207	5	Q27449	Q27449 brugia mala	233	4	66.7	224	5	Q9N4F7	Q9n4f7 caenorhabdi
161	4	66.7	207	9	O80124	O80124 bacterioph	234	4	66.7	225	10	Q9LI49	Q9li49 oryza sativ
162	4	66.7	207	9	Q858N9	Q858n9 lactococcus	235	4	66.7	225	11	Q8R2Z2	Q8r2z2 mus musculu

236	4	66.7	225	11	Q9DLJ5	Q9d1j5 mus musculu	309	4	66.7	257	16	Q89GU8	Q89gu8 bradyrhizob
237	4	66.7	225	11	Q8VCR5	Q8vcr5 mus musculu	310	4	66.7	258	10	Q9FG08	Q9fg08 arabadopsis
238	4	66.7	227	16	Q8VXS7	Q8vxs7 streptomyce	311	4	66.7	258	10	Q8H4P3	Q8h4p3 oryza sativ
239	4	66.7	227	16	Q87XG3	Q87xg3 pseudomonas	312	4	66.7	260	16	Q9I4A3	Q9i4a3 pseudomonas
240	4	66.7	228	2	Q8KZT2	Q8kzt2 rhodococcus	313	4	66.7	261	2	Q9AQG7	Q9agg7 caldicellul
241	4	66.7	228	2	Q9L639	Q9l639 prochloroco	314	4	66.7	261	16	Q55715	Q55715 synechocyst
242	4	66.7	228	16	Q8EL80	Q8el80 oceanobacil	315	4	66.7	261	16	Q829X4	Q829x4 streptomyce
243	4	66.7	228	16	Q8EF09	Q8ef09 shewanella	316	4	66.7	262	2	Q8KZ64	Q8kz64 uncultured
244	4	66.7	228	16	Q7V1B1	Q7vlb1 prochloroco	317	4	66.7	262	16	Q8DAU8	Q8dau8 vibrio vuln
245	4	66.7	230	16	Q8XYP2	Q8xyp2 ralstonia s	318	4	66.7	262	16	Q7U3N7	Q7u3n7 synechococc
246	4	66.7	230	16	Q8PRE3	Q8pre3 xanthomonas	319	4	66.7	263	10	Q9FR36	Q9fr36 glycine max
247	4	66.7	230	16	Q8PEG2	Q8peg2 xanthomonas	320	4	66.7	263	11	Q9EPB6	Q9epb6 mus musculu
248	4	66.7	232	5	Q8INX8	Q8inx8 drosophila	321	4	66.7	263	11	Q9QZY1	Q9qzy1 mus musculu
249	4	66.7	232	16	Q8XPW6	Q8xpw6 ralstonia s	322	4	66.7	263	16	Q9AAP8	Q9aap8 caulobacter
250	4	66.7	232	16	Q82JK5	Q82jk5 streptomyce	323	4	66.7	266	5	Q9TZ29	Q9tzz9 caenorhabdi
251	4	66.7	232	16	Q82GK9	Q82gk9 streptomyce	324	4	66.7	266	5	Q94285	Q94285 caenorhabdi
252	4	66.7	233	3	Q9C172	Q9c172 beauveria b	325	4	66.7	266	16	Q86750	Q86750 streptomyce
253	4	66.7	233	16	Q7VCF4	Q7vcf4 prochloroco	326	4	66.7	267	16	Q89CD4	Q89cd4 bradyrhizob
254	4	66.7	234	16	Q8PP87	Q8pp87 xanthomonas	327	4	66.7	268	16	Q7UF94	Q7uf94 rhodopirell
255	4	66.7	234	16	Q9X897	Q9x897 streptomyce	328	4	66.7	269	4	Q8NEB8	Q8ne88 homo sapien
256	4	66.7	235	13	Q7ZZ94	Q7zz94 brachydanio	329	4	66.7	272	4	Q8N712	Q8n712 homo sapien
257	4	66.7	236	2	Q08385	Q08385 rhodobacter	330	4	66.7	272	5	Q8MTV2	Q8mtv2 drosophila
258	4	66.7	236	2	Q9L8J4	Q9l8j4 rhodospiril	331	4	66.7	272	16	Q99XX1	Q99xx1 streptococc
259	4	66.7	236	5	Q8IR59	Q8ir59 drosophila	332	4	66.7	272	16	Q8K5R2	Q8k5r2 streptococc
260	4	66.7	237	3	Q8NJJ2	Q8njy2 aspergillus	333	4	66.7	273	10	Q94JM4	Q94jm4 arabadopsis
261	4	66.7	238	16	Q8EM85	Q8em85 oceanobacil	334	4	66.7	273	10	Q94OD6	Q94od6 arabadopsis
262	4	66.7	239	16	Q9A5L5	Q9a5l5 caulobacter	335	4	66.7	273	16	Q9K152	Q9k152 neisseria m
263	4	66.7	239	16	Q98LF5	Q98lf5 rhizobium l	336	4	66.7	273	16	Q9JSS7	Q9jss7 neisseria m
264	4	66.7	240	3	Q8NJZ1	Q8njz1 bionectria	337	4	66.7	273	16	Q8NZA1	Q8nza1 streptococc
265	4	66.7	240	5	Q86H62	Q86h62 dictyosteli	338	4	66.7	273	16	Q8DS06	Q8ds06 streptococc
266	4	66.7	240	16	Q9PFU7	Q9pfu7 xylella fas	339	4	66.7	275	2	Q8KLX7	Q8klx7 pseudomonas
267	4	66.7	240	16	Q8YCS1	Q8ycs1 brucella me	340	4	66.7	275	10	Q65710	Q65710 arabadopsis
268	4	66.7	240	16	Q8FVK4	Q8fvk4 brucella su	341	4	66.7	275	12	Q7TGA4	Q7tga4 equine arte
269	4	66.7	240	16	Q87B76	Q87b76 xylella fas	342	4	66.7	275	12	Q7TGA2	Q7tga2 equine arte
270	4	66.7	241	2	Q9AKM2	Q9akm2 rickettsia	343	4	66.7	275	12	Q7TGA1	Q7tga1 equine arte
271	4	66.7	241	2	Q9AKG6	Q9akg6 rickettsia	344	4	66.7	275	12	Q7TGA0	Q7tga0 equine arte
272	4	66.7	241	16	Q92IJ8	Q92ij8 rickettsia	345	4	66.7	275	12	Q7TG99	Q7tg99 equine arte
273	4	66.7	242	3	Q9P8A6	Q9p8a6 agaricus bi	346	4	66.7	275	12	Q7TG98	Q7tg98 equine arte
274	4	66.7	242	5	Q8IGP9	Q8igp9 drosophila	347	4	66.7	276	16	Q9PDL1	Q9pd11 xylella fas
275	4	66.7	242	10	Q8GT53	Q8gt53 hordeum vul	348	4	66.7	276	16	Q9PCS9	Q9pcs9 xylella fas
276	4	66.7	243	16	Q9JYR4	Q9jyr4 neisseria m	349	4	66.7	276	16	Q9CDA2	Q9cda2 mycobacteri
277	4	66.7	243	16	Q8YC11	Q8yc11 brucella me	350	4	66.7	276	16	Q877P0	Q877p0 xylella fas
278	4	66.7	243	16	Q7UTZ6	Q7utz6 rhodopirell	351	4	66.7	276	16	Q7UTG7	Q7utg7 rhodopirell
279	4	66.7	244	4	Q8IVB3	Q8ivb3 homo sapien	352	4	66.7	277	2	Q8GLB8	Q8glb8 xanthomonas
280	4	66.7	244	16	Q836D4	Q836d4 enterococcu	353	4	66.7	277	16	Q8UFC2	Q8ufc2 agrobacteri
281	4	66.7	245	16	Q92KJ4	Q92kj4 rhizobium m	354	4	66.7	277	16	Q92QE0	Q92qe0 rhizobium m
282	4	66.7	246	5	Q9UAV4	Q9uav4 caenorhabdi	355	4	66.7	277	16	Q88XJ0	Q88xj0 lactobacill
283	4	66.7	246	16	Q8E308	Q8e308 streptococc	356	4	66.7	278	16	P74248	P74248 synechocyst
284	4	66.7	246	16	Q8DX86	Q8dx86 streptococc	357	4	66.7	280	13	Q8UVY9	Q8uvy9 brachydanio
285	4	66.7	246	16	Q8CWD6	Q8cwd6 escherichia	358	4	66.7	280	16	Q8YW13	Q8yw13 anabaena sp
286	4	66.7	246	16	Q87VQ5	Q87vq5 pseudomonas	359	4	66.7	280	16	P72049	P72049 mycobacteri
287	4	66.7	246	16	Q83DC4	Q83dc4 coxiella bu	360	4	66.7	280	16	Q7TVN9	Q7tvn9 mycobacteri
288	4	66.7	247	5	Q9VEZ4	Q9vez4 drosophila	361	4	66.7	280	16	Q7TTZ6	Q7ttz6 rhodopirell
289	4	66.7	247	16	Q97P63	Q97p63 streptococc	362	4	66.7	281	2	Q30796	Q30796 methylobact
290	4	66.7	247	16	Q8DS03	Q8ds03 streptococc	363	4	66.7	282	5	Q9BL05	Q9bl05 caenorhabdi
291	4	66.7	249	16	Q99XW9	Q99xw9 streptococc	364	4	66.7	282	16	Q8X7K0	Q8x7k0 escherichia
292	4	66.7	249	16	Q8NZ99	Q8nz99 streptococc	365	4	66.7	282	16	Q8FG09	Q8fg09 escherichia
293	4	66.7	249	16	Q8K5R0	Q8k5r0 streptococc	366	4	66.7	282	16	Q83QZ3	Q83qz3 shigella fl
294	4	66.7	249	16	Q7ULK2	Q7ulk2 rhodopirell	367	4	66.7	284	2	Q9R9Y3	Q9r9y3 pseudomonas
295	4	66.7	250	1	Q9P9C3	Q9p9c3 uncultured	368	4	66.7	284	16	Q9KJX7	Q9kjsx7 pseudomonas
296	4	66.7	250	10	Q9XGG6	Q9xgg6 pisum sativ	369	4	66.7	285	4	Q9BUI3	Q9bui3 homo sapien
297	4	66.7	250	16	Q8PEX6	Q8pex6 xanthomonas	370	4	66.7	285	4	Q9NXI3	Q9nxi3 homo sapien
298	4	66.7	250	16	Q8NR79	Q8nr79 corynebacte	371	4	66.7	285	16	Q8XTZ3	Q8xtz3 ralstonia s
299	4	66.7	250	17	Q8TUH9	Q8tuh9 methanosarc	372	4	66.7	286	16	Q9KEF2	Q9kef2 bacillus ha
300	4	66.7	251	10	Q9LXL9	Q9lk19 vitis berla	373	4	66.7	287	2	Q30655	Q30655 azotobacter
301	4	66.7	251	10	Q7XXR0	Q7xxr0 oryza sativ	374	4	66.7	289	16	Q8ZNQ5	Q8znq5 salmonella
302	4	66.7	251	16	Q8DNP5	Q8dnp5 streptococc	375	4	66.7	289	16	Q8Z5G0	Q8z5g0 salmonella
303	4	66.7	254	16	Q8P3I2	Q8p3i2 xanthomonas	376	4	66.7	289	16	Q83T59	Q83t59 salmonella
304	4	66.7	255	16	Q7WLJ7	Q7wlj7 bordetella	377	4	66.7	290	2	Q59078	Q59078 alteromonas
305	4	66.7	255	16	Q7W849	Q7w849 bordetella	378	4	66.7	290	12	Q88899	Q88899 tobacco rat
306	4	66.7	255	16	Q7VX82	Q7vx82 bordetella	379	4	66.7	291	11	Q811J1	Q811j1 mus musculu
307	4	66.7	256	2	Q9L9V0	Q9l9v0 chromatium	380	4	66.7	292	5	Q7YVN6	Q7yvn6 trypanosoma
308	4	66.7	257	16	Q9X787	Q9x787 mycobacteri	381	4	66.7	292	16	Q92VR3	Q92vr3 rhizobium m

382	4	66.7	292	16	Q89RJ5	Q89rj5 bradyrhizob	455	4	66.7	325	2	Q8VQC9	Q8vqc9 myxococcus
383	4	66.7	293	10	Q93V35	Q93v35 oryza sativ	456	4	66.7	325	2	Q8RMH1	Q8rmh1 acetobacter
384	4	66.7	293	10	Q7XKG4	Q7xkg4 oryza sativ	457	4	66.7	325	5	O17095	O17095 caenorhabdi
385	4	66.7	293	16	Q9A7P0	Q9a7p0 caulobacter	458	4	66.7	325	16	Q8DSQ6	Q8dsq6 streptococc
386	4	66.7	293	16	Q9EWV0	Q9ewv0 streptomyc	459	4	66.7	325	16	Q89DB4	Q89db4 bradyrhizob
387	4	66.7	293	16	Q7U5G6	Q7u5g6 synecchococ	460	4	66.7	328	4	Q9UJ71	Q9uj71 homo sapien
388	4	66.7	294	16	Q9KVV5	Q9kvv5 vibrio chol	461	4	66.7	328	16	Q9WXR6	Q9wxr6 thermotoga
389	4	66.7	295	4	Q96RS2	Q96rs2 homo sapien	462	4	66.7	328	16	Q8DBH2	Q8dbh2 vibrio vuln
390	4	66.7	295	4	Q86VC0	Q86vc0 homo sapien	463	4	66.7	328	16	Q7UT80	Q7ut80 rhodopirell
391	4	66.7	295	11	Q9CY13	Q9cy13 mus musculu	464	4	66.7	328	16	Q7UMG3	Q7umg3 rhodopirell
392	4	66.7	295	11	Q91V31	Q91v31 m 13 days e	465	4	66.7	330	2	P72440	P72440 streptover
393	4	66.7	295	16	Q883H4	Q883h4 pseudomonas	466	4	66.7	330	13	Q7ZW50	Q7zw50 brachydanio
394	4	66.7	295	16	Q81YT6	Q81yt6 bacillus an	467	4	66.7	330	16	Q989M8	Q989m8 rhizobium l
395	4	66.7	295	16	Q813Z4	Q813z4 bacillus ce	468	4	66.7	330	16	Q926E3	Q926e3 rhizobium m
396	4	66.7	295	16	Q813Z4	Q813z4 bacillus ce	469	4	66.7	330	16	Q9KYH6	Q9kyh6 streptomyc
397	4	66.7	297	2	Q52689	Q52689 rhodobacter	470	4	66.7	331	16	Q833W8	Q833w8 enterococcu
398	4	66.7	297	2	Q30730	Q30730 rhodobacter	471	4	66.7	331	16	Q7UW49	Q7uw49 rhodopirell
399	4	66.7	297	11	Q8BG50	Q8bg50 mus musculu	472	4	66.7	332	2	Q9F5R6	Q9f5r6 streptomyc
400	4	66.7	297	16	Q98B17	Q98b17 rhizobium l	473	4	66.7	332	5	Q9W2Q2	Q9w2q2 drosophila
401	4	66.7	298	2	Q8KP31	Q8kp31 agromyces m	474	4	66.7	332	8	Q9T7K6	Q9t7k6 crassostrea
402	4	66.7	298	16	Q9A9G2	Q9a9g2 caulobacter	475	4	66.7	332	10	Q93ZH9	Q93zh9 arabadopsis
403	4	66.7	298	16	Q83JN0	Q83jn0 shigella fl	476	4	66.7	332	16	Q8PPH2	Q8pph2 xanthomonas
404	4	66.7	299	10	Q9LM13	Q9lmi3 arabadopsis	477	4	66.7	332	16	Q8P5D0	Q8p5d0 xanthomonas
405	4	66.7	299	16	Q7V6D1	Q7v6d1 prochloroco	478	4	66.7	332	16	Q87AY2	Q87ay2 xylella fas
406	4	66.7	300	2	Q59248	Q59248 bacillus su	479	4	66.7	333	5	Q9W2J6	Q9w2j6 drosophila
407	4	66.7	300	6	Q9GMP3	Q9gmp3 macaca fasc	480	4	66.7	334	10	Q84MQ0	Q84mq0 oryza sativ
408	4	66.7	300	16	Q9A237	Q9a237 caulobacter	481	4	66.7	334	16	Q9ZBY6	Q9zby6 streptomyc
409	4	66.7	301	16	Q98F65	P96688 bacillus su	482	4	66.7	334	16	Q82FJ3	Q82fj3 streptomyc
410	4	66.7	302	10	Q8LJW6	Q8lf65 rhizobium l	483	4	66.7	335	16	Q989F6	Q989f6 rhizobium l
411	4	66.7	302	16	Q9I670	Q8ljw6 sorghum bic	484	4	66.7	336	4	Q96KQ0	Q96kq0 homo sapien
412	4	66.7	302	16	Q8FYS1	Q9i670 pseudomonas	485	4	66.7	337	2	Q9ZGH3	Q9zgh3 streptomyc
413	4	66.7	303	10	Q9M1K7	Q8fys1 brucella su	486	4	66.7	337	5	P92001	P92001 caenorhabdi
414	4	66.7	304	5	Q9XUN0	Q9mlk7 arabadopsis	487	4	66.7	337	11	Q80UX8	Q80ux8 mus musculu
415	4	66.7	304	16	Q8FDN3	Q9xun0 caenorhabdi	488	4	66.7	337	16	Q7US31	Q7us31 rhodopirell
416	4	66.7	305	16	Q88RH3	Q8fdn3 escherichia	489	4	66.7	338	16	Q9RT55	Q9rt55 deinococcus
417	4	66.7	306	3	Q01086	Q88rh3 pseudomonas	490	4	66.7	338	16	Q8XDE0	Q8xde0 escherichia
418	4	66.7	306	13	Q7ZX07	Q01086 kluveromyc	491	4	66.7	338	16	P73085	P73085 synecchocyst
419	4	66.7	306	16	Q87U52	Q7zx07 xenopus lae	492	4	66.7	339	5	P92002	P92002 caenorhabdi
420	4	66.7	307	2	Q9X9S5	Q87u52 pseudomonas	493	4	66.7	340	16	Q9PGB5	Q9pgb5 xylella fas
421	4	66.7	307	16	Q8YJ28	Q8y9b5 streptomyc	494	4	66.7	341	2	Q8KIP8	Q8kip8 pseudomonas
422	4	66.7	307	16	Q830T5	Q8yj28 brucella me	495	4	66.7	341	16	Q882G1	Q882g1 pseudomonas
423	4	66.7	308	2	Q93R73	Q830t5 enterococcu	496	4	66.7	342	16	Q8UK18	Q8uk18 agrobacteri
424	4	66.7	308	4	Q7Z6L3	Q93r73 streptococc	497	4	66.7	343	2	P72464	P72464 streptomyc
425	4	66.7	308	13	Q803F6	Q7z6l3 homo sapien	498	4	66.7	343	2	Q8KWC9	Q8kwc9 ruegeria sp
426	4	66.7	309	4	Q8N2Y4	Q803f6 brachydanio	499	4	66.7	343	10	Q94LD0	Q94ld0 oryza sativ
427	4	66.7	309	16	Q8P1R0	Q8n2y4 homo sapien	500	4	66.7	343	16	Q983C5	Q983c5 rhizobium l
428	4	66.7	310	2	Q9XBS7	Q8plr0 streptococc	501	4	66.7	343	16	Q8XZ75	Q8xz75 ralstonia s
429	4	66.7	310	3	Q8TGE0	Q9xbs7 zymomonas m	502	4	66.7	343	16	Q7USB9	Q7usb9 rhodopirell
430	4	66.7	310	10	O64924	Q8tge0 aspergillus	503	4	66.7	344	2	Q8KRX3	Q8krx3 streptomyc
431	4	66.7	312	16	Q8XZ21	O64924 zea mays (m	504	4	66.7	344	10	Q9SKL5	Q9skl5 arabadopsis
432	4	66.7	312	16	Q8NZP6	Q8xz21 ralstonia s	505	4	66.7	344	16	O32258	O32258 bacillus su
433	4	66.7	313	16	Q8XG37	Q8nzp6 streptococc	506	4	66.7	344	16	Q7U660	Q7u660 synecchococ
434	4	66.7	313	16	Q88T79	Q8kg37 chlorobium	507	4	66.7	344	17	Q8TII4	Q8tii4 methanosarc
435	4	66.7	314	2	Q9AML6	Q88t79 lactobacill	508	4	66.7	345	2	Q9F620	Q9f620 rhizobium m
436	4	66.7	314	11	Q8BUX9	Q9aml6 edwardsiell	509	4	66.7	345	10	Q8S9T8	Q8s9t8 oryza sativ
437	4	66.7	314	16	Q8FWA9	Q8bux9 mus musculu	510	4	66.7	345	16	Q92RZ1	Q92rz1 rhizobium m
438	4	66.7	315	16	Q87V43	Q8fwa9 brucella su	511	4	66.7	345	16	Q8YGG2	Q8ygg2 brucella me
439	4	66.7	316	2	O69348	Q87v43 pseudomonas	512	4	66.7	345	16	Q8G1F9	Q8glf9 brucella su
440	4	66.7	316	11	Q8VFW9	O69348 rhodococcus	513	4	66.7	346	16	Q88T84	Q88t84 lactobacill
441	4	66.7	317	16	Q55809	Q8vbw9 mus musculu	514	4	66.7	346	2	Q8KY90	Q8ky90 edwardsiell
442	4	66.7	317	16	Q9X273	Q55809 synecchocyst	515	4	66.7	346	2	O32484	O32484 enterobacte
443	4	66.7	318	2	Q53813	Q9x273 thermotoga	516	4	66.7	346	2	O848V3	Q848v3 edwardsiell
444	4	66.7	319	3	O94064	Q53813 shigella bo	517	4	66.7	346	2	Q83WB5	Q83wb5 edwardsiell
445	4	66.7	319	16	Q8NTB5	Q94064 candida alb	518	4	66.7	346	16	Q986J8	Q986j8 rhizobium l
446	4	66.7	320	2	Q84BJ7	Q8ntb5 corynebacte	519	4	66.7	346	16	Q92T78	Q92t78 rhizobium m
447	4	66.7	321	16	Q8U6Y1	Q84bj7 halobacillu	520	4	66.7	346	16	Q8ZKX5	Q8zxx5 salmonella
448	4	66.7	321	16	Q8PK81	Q86ve5 homo sapien	521	4	66.7	346	16	Q8XB03	Q8xb03 escherichia
449	4	66.7	322	16	Q8PK81	Q8u6y1 agrobacteri	522	4	66.7	346	16	Q8CVJ8	Q8cvj8 escherichia
450	4	66.7	323	12	Q9QTE2	Q8pk81 xanthomonas	523	4	66.7	346	16	Q8Z2P5	Q8zzp5 salmonella
451	4	66.7	323	16	Q8XQW6	Q9qte2 marek's dis	524	4	66.7	347	10	Q8GZS9	Q8gzs9 brassica ol
452	4	66.7	324	16	Q8YD70	Q8xqw6 ralstonia s	525	4	66.7	347	17	O29274	O29274 archaeoglob
453	4	66.7	324	16	Q8FV61	Q8yd70 brucella me	526	4	66.7	349	16	Q8DSD3	Q8dsd3 streptococc
454	4	66.7	324	16	Q7U7Y6	Q8fv61 brucella su	527	4	66.7	350	2	Q9RN58	Q9rn58 streptomyc
						Q7u7y6 synecchococ							

528	4	66.7	350	16	Q9L1B2	Q911b2 streptomyce	601	4	66.7	400	16	Q887E6	Q887e6 pseudomonas
529	4	66.7	351	4	Q13539	Q13539 homo sapien	602	4	66.7	400	16	Q82GL5	Q82gl5 streptomyce
530	4	66.7	351	5	Q95X33	Q95x33 caenorhabdi	603	4	66.7	400	16	Q7UTG5	Q7utg5 rhodopirell
531	4	66.7	351	16	Q8P543	Q8p543 xanthomonas	604	4	66.7	401	16	Q8G1G9	Q8glg9 brucella su
532	4	66.7	352	16	Q89F45	Q89f45 bradyrhizob	605	4	66.7	401	16	Q8FRT5	Q8ftr5 corynebacte
533	4	66.7	354	16	Q9HY16	Q9hy16 pseudomonas	606	4	66.7	403	5	Q61866	Q61866 caenorhabdi
534	4	66.7	355	16	Q9FB14	Q9fb14 streptomyce	607	4	66.7	404	2	Q9X5R5	Q9x5r5 streptomyce
535	4	66.7	355	16	Q7UMS6	Q7uma6 rhodopirell	608	4	66.7	404	10	Q94HM3	Q94hm3 oryza sativ
536	4	66.7	356	16	Q8DB65	Q8db65 vibrio vuln	609	4	66.7	404	10	Q7XGI7	Q7xgi7 oryza sativ
537	4	66.7	357	2	Q9RBK8	Q9rbk8 xanthomonas	610	4	66.7	404	16	Q06263	Q06263 mycobacteri
538	4	66.7	357	2	Q83XE8	Q83xe8 xanthomonas	611	4	66.7	404	16	Q8G4W6	Q8g4w6 bifidobacte
539	4	66.7	357	13	Q7ZTN3	Q7ztn3 xenopus lae	612	4	66.7	404	16	Q7TWH6	Q7twh6 mycobacteri
540	4	66.7	357	16	Q8PQC2	Q8pqc2 xanthomonas	613	4	66.7	405	5	Q93789	Q93789 caenorhabdi
541	4	66.7	357	16	Q8PB93	Q8pb93 xanthomonas	614	4	66.7	405	13	Q8UWH2	Q8uwH2 brachydanio
542	4	66.7	358	10	Q8LJH3	Q8ljj3 oryza sativ	615	4	66.7	408	16	Q7WM51	Q7wm51 bordetella
543	4	66.7	358	13	Q9YH17	Q9yhl7 gallus gall	616	4	66.7	409	10	Q9M3F6	Q9m3f6 arabadopsis
544	4	66.7	358	16	Q89PW3	Q89pw3 bradyrhizob	617	4	66.7	410	16	Q7WK41	Q7wk41 bordetella
545	4	66.7	359	2	Q9KW30	Q9kw30 xanthomonas	618	4	66.7	410	16	Q7W8T1	Q7w8t1 bordetella
546	4	66.7	360	2	Q50378	Q50378 mycobacteri	619	4	66.7	410	16	Q7VZ32	Q7vz32 bordetella
547	4	66.7	360	10	Q9SHX9	Q9shx9 arabadopsis	620	4	66.7	410	16	Q7V682	Q7v682 prochloroco
548	4	66.7	360	11	Q8CGB8	Q8cgb8 mus musculu	621	4	66.7	411	5	Q94252	Q94252 caenorhabdi
549	4	66.7	361	16	Q8P955	Q8p955 xanthomonas	622	4	66.7	411	16	Q8U9U2	Q8u9u2 agrobacteri
550	4	66.7	364	6	Q77568	Q77568 saimiri sci	623	4	66.7	411	16	Q925C3	Q92ac3 rhizobium m
551	4	66.7	364	16	Q55548	Q55548 synechocyst	624	4	66.7	411	16	Q9RD79	Q9rd79 streptomyce
552	4	66.7	365	3	Q12291	Q12291 saccharomyc	625	4	66.7	415	10	Q9S1X0	Q9s1x0 arabadopsis
553	4	66.7	369	10	Q8VMX2	Q8vmx2 perilla fru	626	4	66.7	415	13	Q7SXU1	Q7sxu1 brachydanio
554	4	66.7	369	16	Q8G7G2	Q8g7g2 bifidobacte	627	4	66.7	415	16	Q8Z002	Q8z002 anabaena sp
555	4	66.7	371	16	Q9EX41	Q9ex41 streptomyce	628	4	66.7	415	16	Q7UWB0	Q7uwb0 rhodopirell
556	4	66.7	371	17	Q28901	Q28901 archaeoglob	629	4	66.7	416	16	Q7U9Q8	Q7u9q8 synechococc
557	4	66.7	372	5	Q23849	Q23849 dictyosteli	630	4	66.7	417	5	Q8INJ5	Q8inj5 drosophila
558	4	66.7	372	16	Q72682	Q72682 synechocyst	631	4	66.7	417	16	Q53319	Q53319 mycobacteri
559	4	66.7	373	16	Q9ZC00	Q9zc00 streptomyce	632	4	66.7	419	16	Q982K3	Q982k3 rhizobium l
560	4	66.7	373	16	Q8FQAS	Q8fgas corynebacte	633	4	66.7	419	16	Q9WZ64	Q9wz64 thermotoga
561	4	66.7	374	2	Q9X471	Q9x471 streptomyce	634	4	66.7	420	6	Q95K62	Q95k62 macaca fasc
562	4	66.7	374	16	Q7TX42	Q7tx42 mycobacteri	635	4	66.7	421	5	Q9GPA6	Q9gpa6 strongyloce
563	4	66.7	375	17	Q8ZSS9	Q8zss9 pyrobaculum	636	4	66.7	421	16	Q8FPI1	Q8fpi1 corynebacte
564	4	66.7	376	3	Q9UVL4	Q9uvl4 penicillium	637	4	66.7	423	8	Q05896	Q05896 beta vulgar
565	4	66.7	377	16	Q8PD85	Q8pd85 xanthomonas	638	4	66.7	423	10	Q9FH91	Q9fh91 arabadopsis
566	4	66.7	379	16	Q8DLR0	Q8dlr0 synechococc	639	4	66.7	424	16	Q8ZAH6	Q8zah6 yersinia pe
567	4	66.7	380	16	Q8ZNL6	Q8znl6 salmonella	640	4	66.7	425	16	Q8XUM9	Q8xum9 ralstonia s
568	4	66.7	380	16	Q881J6	Q881j6 pseudomonas	641	4	66.7	426	12	Q8JL38	Q8jl38 virus phich
569	4	66.7	380	16	Q8Z5A2	Q8z5a2 salmonella	642	4	66.7	427	2	Q9RHZ6	Q9rhz6 alicyclobac
570	4	66.7	381	16	Q983R9	Q983r9 rhizobium l	643	4	66.7	428	16	Q7V028	Q7v028 prochloroco
571	4	66.7	383	16	Q9HY78	Q9hy78 pseudomonas	644	4	66.7	429	4	Q9H7V8	Q9h7v8 homo sapien
572	4	66.7	383	16	Q82GR3	Q82gr3 streptomyce	645	4	66.7	429	5	Q95Y50	Q95y50 caenorhabdi
573	4	66.7	384	12	Q9E6R3	Q9e6r3 turkey herp	646	4	66.7	429	16	Q50004	Q50004 mycobacteri
574	4	66.7	384	16	Q8PCC5	Q8pc5 xanthomonas	647	4	66.7	429	16	Q7VA54	Q7va54 prochloroco
575	4	66.7	384	16	Q82MF1	Q82mf1 streptomyce	648	4	66.7	429	16	Q7TUN0	Q7tun0 prochloroco
576	4	66.7	385	5	Q9BIH6	Q9bih6 anopheles g	649	4	66.7	430	16	Q9ADH5	Q9adh5 streptomyce
577	4	66.7	387	16	Q8XR48	Q8xr48 ralstonia s	650	4	66.7	430	16	Q8CW12	Q8cwi2 yersinia pe
578	4	66.7	387	16	Q7WIA8	Q7wia8 bordetella	651	4	66.7	430	16	Q7WDQ5	Q7wdq5 bordetella
579	4	66.7	387	16	Q7W6D9	Q7w6d9 bordetella	652	4	66.7	430	16	Q7W0J5	Q7w0j5 bordetella
580	4	66.7	388	10	Q9LUP8	Q9lup8 arabadopsis	653	4	66.7	430	16	Q7V5R7	Q7v5r7 prochloroco
581	4	66.7	390	16	Q9ABM5	Q9abm5 caulobacter	654	4	66.7	431	3	Q8NIP0	Q8nip0 cryptococcu
582	4	66.7	391	13	Q7T1J4	Q7t1j4 brachydanio	655	4	66.7	431	5	Q8SWI0	Q8swi0 encephalito
583	4	66.7	392	2	Q84H77	Q84h77 rhodococcus	656	4	66.7	431	10	Q84S41	Q84s41 oryza sativ
584	4	66.7	394	4	Q7Z593	Q7z593 homo sapien	657	4	66.7	432	10	Q7XT41	Q7xt41 oryza sativ
585	4	66.7	395	2	Q9X412	Q9x412 chlamyidophi	658	4	66.7	433	16	Q8G5Q6	Q8g5q6 bifidobacte
586	4	66.7	395	2	Q9S6B3	Q9s6b3 chlamydia p	659	4	66.7	434	16	Q82K42	Q82k42 streptomyce
587	4	66.7	395	16	Q8YGF2	Q8ygf2 brucella me	660	4	66.7	436	16	Q81ZV9	Q81zv9 streptomyce
588	4	66.7	395	16	Q88KC3	Q88kc3 pseudomonas	661	4	66.7	437	2	Q7X410	Q7x4i0 pseudomonas
589	4	66.7	396	16	Q7WN48	Q7wn48 bordetella	662	4	66.7	438	16	Q8Y309	Q8y309 ralstonia s
590	4	66.7	396	16	Q7WBM4	Q7wbm4 bordetella	663	4	66.7	438	16	Q07183	Q07183 mycobacteri
591	4	66.7	397	16	Q89S40	Q89s40 bradyrhizob	664	4	66.7	438	16	Q7TY44	Q7ty44 mycobacteri
592	4	66.7	398	2	Q8KQ10	Q8kgi0 rhodococcus	665	4	66.7	439	2	Q84BF1	Q84bf1 xanthomonas
593	4	66.7	398	4	Q96KQ1	Q96kq1 homo sapien	666	4	66.7	440	16	Q82LW1	Q82lw1 streptomyce
594	4	66.7	398	4	Q8WYN0	Q8wyn0 homo sapien	667	4	66.7	441	10	Q9SI18	Q9si18 arabadopsis
595	4	66.7	398	12	Q9IBX1	Q9ibx1 turkey herp	668	4	66.7	443	16	Q9ZBI7	Q9zbi7 streptomyce
596	4	66.7	399	16	Q8Z0S1	Q8z0s1 anabaena sp	669	4	66.7	445	16	Q9KPB7	Q9kpb7 vibrio chol
597	4	66.7	400	13	Q90YD6	Q90yd6 xenopus tro	670	4	66.7	448	16	Q88KW1	Q88kw1 pseudomonas
598	4	66.7	400	13	Q73818	Q73818 xenopus lae	671	4	66.7	449	16	Q06407	Q06407 mycobacteri
599	4	66.7	400	13	Q91703	Q91703 xenopus lae	672	4	66.7	449	16	Q7UIT6	Q7ult6 mycobacteri
600	4	66.7	400	16	Q8YUD9	Q8yud9 anabaena sp	673	4	66.7	450	5	Q8SXC2	Q8sxc2 drosophila

674	4	66.7	450	5	Q8T994	Q8t994 drosophila	747	4	66.7	477	16	Q92VE6	Q92ve6 rhizobium m
675	4	66.7	450	16	O33236	O33236 mycobacteri	748	4	66.7	477	16	Q7UUW0	Q7uuw0 rhodopirell
676	4	66.7	450	16	Q9RJ91	Q9xj91 streptomyce	749	4	66.7	477	17	Q97OV3	Q970v3 sulfolobus
677	4	66.7	450	16	Q7TY07	Q7ty07 mycobacteri	750	4	66.7	478	2	Q8GIE3	Q8gie3 mycoplasma
678	4	66.7	451	2	Q56758	Q56758 xanthobacte	751	4	66.7	478	2	Q8GIE0	Q8gie0 mycoplasma
679	4	66.7	451	16	Q7UMJ4	Q7umj4 rhodopirell	752	4	66.7	478	4	Q9H0J7	Q9h0j7 homo sapien
680	4	66.7	452	2	O66239	O66239 escherichia	753	4	66.7	478	10	Q7XJ05	Q7xj05 oryza sativ
681	4	66.7	452	2	O66235	O66235 escherichia	754	4	66.7	480	16	Q885S8	Q885s8 pseudomonas
682	4	66.7	452	2	O70051	O70051 klebsiella	755	4	66.7	480	16	Q7UY49	Q7uy49 rhodopirell
683	4	66.7	452	5	O61918	O61918 caenorhabdi	756	4	66.7	481	16	Q8DII4	Q8di14 synechococc
684	4	66.7	452	16	Q8ZL19	Q8z119 salmonella	757	4	66.7	482	16	Q82ZN7	Q82zn7 enterococcu
685	4	66.7	452	16	Q8Z2K1	Q8z2k1 salmonella	758	4	66.7	482	16	Q82CP3	Q82cp3 streptomyce
686	4	66.7	452	16	Q82VS7	Q82vs7 nitrosomona	759	4	66.7	483	17	Q9UX28	Q9ux28 sulfolobus
687	4	66.7	452	16	Q81RJ45	Q81r45 bacillus an	760	4	66.7	484	5	Q9XUA8	Q9xua8 caenorhabdi
688	4	66.7	453	2	Q9Z9T3	Q9z9t3 bacillus ha	761	4	66.7	484	16	Q8XDJ5	Q8xdj5 escherichia
689	4	66.7	453	5	Q9VZ57	Q9vz57 drosophila	762	4	66.7	484	16	Q83II9	Q83ii9 shigella fl
690	4	66.7	453	12	Q67215	Q67215 influenzavi	763	4	66.7	486	13	Q804D8	Q804d8 bufo arenar
691	4	66.7	453	12	Q67217	Q67217 influenzavi	764	4	66.7	487	10	Q7XVI9	Q7xvi9 oryza sativ
692	4	66.7	453	12	Q67216	Q67216 influenzavi	765	4	66.7	487	16	Q8DB92	Q8db92 vibrio vuln
693	4	66.7	453	16	Q8KG44	Q8kg44 chlorobium	766	4	66.7	489	5	Q8IRK2	Q8irk2 drosophila
694	4	66.7	454	2	Q9RMU5	Q9rmu5 klebsiella	767	4	66.7	489	16	P96223	P96223 mycobacteri
695	4	66.7	454	10	Q40100	Q40100 ipomoea tri	768	4	66.7	489	16	Q7UTD0	Q7utd0 rhodopirell
696	4	66.7	454	12	Q8JUJ4	Q8juu4 influenza a	769	4	66.7	489	16	Q7TVI2	Q7tvi2 mycobacteri
697	4	66.7	457	10	Q84KH1	Q84kh1 triticum mo	770	4	66.7	491	4	Q9H8X2	Q9h8x2 homo sapien
698	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	771	4	66.7	491	16	Q9I218	Q9i218 pseudomonas
699	4	66.7	457	16	Q8G5A0	Q8g5a0 bifidobacte	772	4	66.7	492	5	Q9WLH3	Q9wlh3 drosophila
700	4	66.7	457	16	Q7ULE0	Q7ule0 rhodopirell	773	4	66.7	495	12	Q9J840	Q9j840 spodoptera
701	4	66.7	458	10	Q9SH74	Q9sh74 arabidopsis	774	4	66.7	495	16	Q88G57	Q88g57 pseudomonas
702	4	66.7	458	16	Q87J61	Q87j61 vibrio para	775	4	66.7	498	8	Q9B929	Q9b929 krادibia wa
703	4	66.7	460	16	Q88F35	Q88f35 pseudomonas	776	4	66.7	498	16	Q9A9H5	Q9a9h5 caulobacter
704	4	66.7	461	2	Q93TV6	Q93tv6 pseudomonas	777	4	66.7	498	16	Q88A20	Q88a20 pseudomonas
705	4	66.7	462	16	Q8X5T1	Q8x5t1 escherichia	778	4	66.7	499	10	Q7XU35	Q7xu35 oryza sativ
706	4	66.7	462	16	Q8FCM4	Q8fcm4 escherichia	779	4	66.7	503	3	Q9Y7D3	Q9y7d3 aspergillus
707	4	66.7	463	4	Q9NQG6	Q9ncg6 homo sapien	780	4	66.7	503	10	Q8RYT0	Q8ryt0 oryza sativ
708	4	66.7	463	11	Q8C4Y9	Q8c4y9 mus musculu	781	4	66.7	507	16	Q8UG94	Q8ug94 agrobacteri
709	4	66.7	463	11	Q8BGV8	Q8bgv8 mus musculu	782	4	66.7	507	16	Q8CK16	Q8ck16 streptomyce
710	4	66.7	463	16	Q9KOT7	Q9kot7 neisseria m	783	4	66.7	507	16	Q829F0	Q829f0 streptomyce
711	4	66.7	463	16	Q9JT31	Q9jt31 neisseria m	784	4	66.7	509	16	Q98KE4	Q98ke4 rhizobium l
712	4	66.7	463	16	Q88HK6	Q88hk6 pseudomonas	785	4	66.7	510	3	Q8X0B2	Q8x0b2 neurospora
713	4	66.7	464	12	Q9WMK8	Q9wmk8 influenzavi	786	4	66.7	511	2	Q93FV8	Q93fv8 chlamydia t
714	4	66.7	464	12	Q9WMK7	Q9wmk7 influenzavi	787	4	66.7	514	12	Q9QAH0	Q9qah0 raspberry r
715	4	66.7	464	16	P73249	P73249 synechocyst	788	4	66.7	514	12	Q9QAG9	Q9qag9 raspberry r
716	4	66.7	464	16	Q92E77	Q92e77 listeria in	789	4	66.7	514	12	Q9QAH4	Q9qah4 raspberry r
717	4	66.7	464	16	Q8Y9F4	Q8y9f4 listeria mo	790	4	66.7	514	12	Q9QAG8	Q9qag8 raspberry r
718	4	66.7	465	16	Q8FAJ3	Q8faj3 escherichia	791	4	66.7	514	12	Q9QAH3	Q9qah3 raspberry r
719	4	66.7	466	16	Q9K615	Q9k615 bacillus ha	792	4	66.7	514	12	Q9QAH5	Q9qah5 raspberry r
720	4	66.7	467	3	Q871Y9	Q87ly9 neurospora	793	4	66.7	514	16	Q8CK14	Q8ck14 streptomyce
721	4	66.7	467	10	Q9SIW9	Q9siw9 arabidopsis	794	4	66.7	515	10	Q94CQ3	Q94cq3 oryza sativ
722	4	66.7	468	5	Q9VTX5	Q9vtx5 drosophila	795	4	66.7	516	10	Q80726	Q80726 arabidopsis
723	4	66.7	468	5	O18358	O18358 drosophila	796	4	66.7	516	10	Q8RY31	Q8ry31 arabidopsis
724	4	66.7	468	16	Q7UJH9	Q7ujh9 rhodopirell	797	4	66.7	517	10	Q9SFG3	Q9sf93 arabidopsis
725	4	66.7	469	12	Q9IBI1	Q9ibi1 influenza a	798	4	66.7	519	3	O59944	O59944 ceriporiops
726	4	66.7	469	12	Q8JSE0	Q8jse0 influenza a	799	4	66.7	520	3	Q871C4	Q871c4 neurospora
727	4	66.7	469	12	Q8JSD9	Q8jsd9 influenza a	800	4	66.7	523	10	Q8S9A1	Q8s9a1 phaseolus a
728	4	66.7	470	12	Q8JWH6	Q8jmh6 influenza a	801	4	66.7	525	5	Q9BMD6	Q9bmd6 antheraea p
729	4	66.7	470	12	Q8JMH7	Q8jmh7 influenza a	802	4	66.7	525	16	Q82HM9	Q82hm9 streptomyce
730	4	66.7	470	16	Q8A335	Q8a335 bacteroides	803	4	66.7	526	13	Q9I910	Q9i910 xenopus lae
731	4	66.7	470	16	Q82JU7	Q82ju7 streptomyce	804	4	66.7	527	5	Q9XVN8	Q9xvn8 caenorhabdi
732	4	66.7	470	16	Q7WKK9	Q7wkk9 bordetella	805	4	66.7	527	5	O76383	O76383 caenorhabdi
733	4	66.7	470	16	Q7W964	Q7w964 bordetella	806	4	66.7	528	16	Q7VEH5	Q7veh5 prochloroco
734	4	66.7	470	16	Q7VVM0	Q7vvw0 bordetella	807	4	66.7	528	16	Q7V9A9	Q7v9a9 prochloroco
735	4	66.7	471	2	Q59427	Q59427 escherichia	808	4	66.7	528	16	Q7V3N7	Q7v3n7 prochloroco
736	4	66.7	471	2	O66228	O66228 escherichia	809	4	66.7	528	16	Q7UA53	Q7ua53 synechococc
737	4	66.7	471	16	Q7UVM6	Q7uvm6 rhodopirell	810	4	66.7	530	16	Q88PG6	Q88pg6 pseudomonas
738	4	66.7	474	2	Q54408	Q54408 streptomyce	811	4	66.7	532	16	Q9I2X5	Q9i2x5 pseudomonas
739	4	66.7	474	2	Q83XP2	Q83xp2 streptomyce	812	4	66.7	532	16	Q7ULG5	Q7ulg5 rhodopirell
740	4	66.7	474	16	Q8PQ56	Q8pq56 xanthomonas	813	4	66.7	533	5	Q94677	Q94677 plasmodium
741	4	66.7	474	16	Q9RDG7	Q9rdg7 streptomyce	814	4	66.7	534	2	Q9ZAW1	Q9zaw1 chlamydrophi
742	4	66.7	476	16	Q8ZK90	Q8zk90 salmonella	815	4	66.7	534	10	Q8RWH6	Q8rwh6 arabidopsis
743	4	66.7	476	16	Q8Z172	Q8z172 salmonella	816	4	66.7	534	11	Q9D5W9	Q9d5w9 mus musculu
744	4	66.7	477	5	Q95VY4	Q95vy4 aedes aegyp	817	4	66.7	534	16	P74381	P74381 synechocyst
745	4	66.7	477	10	Q9FPT3	Q9fpt3 arabidopsis	818	4	66.7	534	16	Q8P735	Q8p735 xanthomonas
746	4	66.7	477	10	Q84WC6	Q84wc6 arabidopsis	819	4	66.7	534	16	Q93GX7	Q93gx7 streptomyce

820	4	66.7	534	17	Q8PSW2	Q8psw2 methanosarc	893	4	66.7	606	13	Q9I916	Q9i916 brachydanio
821	4	66.7	535	16	Q8G5P4	Q8g5p4 bifidobacte	894	4	66.7	606	13	Q7ZU27	Q7zu27 brachydanio
822	4	66.7	537	16	O05459	O05459 mycobacteri	895	4	66.7	606	16	Q8FB08	Q8fb08 escherichia
823	4	66.7	537	16	Q7TVF5	Q7tvf5 mycobacteri	896	4	66.7	606	16	Q82KE7	Q82ke7 streptomyce
824	4	66.7	538	11	Q8C9K6	Q8c9k6 mus musculu	897	4	66.7	607	10	Q9LQJ7	Q9lgj7 oryza sativ
825	4	66.7	542	5	O77059	O77059 drosophila	898	4	66.7	608	12	Q80MY5	Q80my5 human cytom
826	4	66.7	542	5	Q9TYA0	Q9tya0 drosophila	899	4	66.7	608	12	Q80MY1	Q80my1 human cytom
827	4	66.7	542	16	Q8KBZ8	Q8kbz8 chlorobium	900	4	66.7	609	5	Q95X10	Q95x10 drosophila
828	4	66.7	544	2	Q8KN49	Q8kn49 sphingobium	901	4	66.7	609	11	Q8K4B2	Q8k4b2 mus musculu
829	4	66.7	544	5	Q27659	Q27659 giardia lam	902	4	66.7	609	11	Q8C7U8	Q8c7u8 mus musculu
830	4	66.7	545	12	P89475	P89475 herpes simp	903	4	66.7	609	11	Q8CE40	Q8ce40 mus musculu
831	4	66.7	546	16	Q8U6I5	Q8u6i5 agrobacteri	904	4	66.7	609	17	Q97WE1	Q97we1 sulfolobus
832	4	66.7	547	2	Q933I7	Q933i7 chlamydia t	905	4	66.7	611	10	Q84TA3	Q84ta3 oryza sativ
833	4	66.7	547	10	Q8H1F0	Q8hlfo arabidopsis	906	4	66.7	612	8	Q8HMF9	Q8hmf9 sirembo imb
834	4	66.7	547	10	Q8SAW6	Q8saw6 oryza sativ	907	4	66.7	612	8	Q8HLZ1	Q8hlz1 melanotaeni
835	4	66.7	547	10	Q8RXX4	Q8rxk4 arabidopsis	908	4	66.7	613	16	Q8YN26	Q8yn26 anabaena sp
836	4	66.7	547	10	Q7XGL6	Q7xgl6 oryza sativ	909	4	66.7	615	16	Q7UJS7	Q7ujst rhodopirell
837	4	66.7	547	16	Q9RZJ4	Q9rzj4 deinococcus	910	4	66.7	616	13	Q90WY1	Q90wy1 xenopus lae
838	4	66.7	548	17	Q9HPQ3	Q9hpn3 halobacteri	911	4	66.7	617	16	Q81YD8	Q8lyd8 bacillus su
839	4	66.7	550	3	Q9C124	Q9cl24 pichia past	912	4	66.7	620	16	Q8FZX3	Q8fzx3 brucella su
840	4	66.7	550	5	Q9NG18	Q9ngl8 trypanosoma	913	4	66.7	621	13	Q8QG61	Q8qg61 gallus gall
841	4	66.7	553	5	Q86N96	Q86n96 leishmania	914	4	66.7	621	16	Q7UT91	Q7ut91 rhodopirell
842	4	66.7	553	10	Q9T0J7	Q9t0j7 arabidopsis	915	4	66.7	623	5	Q9V534	Q9v534 drosophila
843	4	66.7	553	16	Q8ZIH3	Q8zih3 yersinia pe	916	4	66.7	626	4	Q8N491	Q8n491 homo sapien
844	4	66.7	553	16	Q8XWP8	Q8xwp8 ralstonia s	917	4	66.7	627	10	Q9MAS7	Q9mas7 arabidopsis
845	4	66.7	553	16	Q8CZP9	Q8czp9 yersinia pe	918	4	66.7	627	16	Q7UKV6	Q7ukv6 rhodopirell
846	4	66.7	554	16	Q9PJV0	Q9pju0 chlamydia m	919	4	66.7	628	5	Q9GV14	Q9gv14 hydra magni
847	4	66.7	556	10	Q94CQ2	Q94cq2 oryza sativ	920	4	66.7	629	16	Q930A0	Q930a0 rhizobium m
848	4	66.7	556	13	Q9I9I7	Q9i9i7 brachydanio	921	4	66.7	630	2	O87110	O87110 comamonas a
849	4	66.7	556	16	O34650	O34650 bacillus su	922	4	66.7	631	16	Q8ZQU8	Q8zqu8 salmonella
850	4	66.7	557	2	Q9AIS7	Q9ais7 chlamydomphi	923	4	66.7	632	8	Q7YMD6	Q7ymd6 aneilema ca
851	4	66.7	557	10	Q94KV1	Q94kv1 chlamydomon	924	4	66.7	636	4	Q7Z7P1	Q7z7p1 homo sapien
852	4	66.7	557	16	Q8A5P5	Q8a5p5 bacteroides	925	4	66.7	636	10	Q84Z86	Q84z86 oryza sativ
853	4	66.7	557	16	Q834P1	Q834p1 enterococcu	926	4	66.7	637	5	O45915	O45915 caenorhabdi
854	4	66.7	558	2	Q9R9W8	Q9r9w8 pseudomonas	927	4	66.7	637	5	Q9GZ30	Q9gz30 trypanosoma
855	4	66.7	559	16	Q8PQT4	Q8pqt4 xanthomonas	928	4	66.7	637	10	Q94CQ4	Q94cq4 oryza sativ
856	4	66.7	560	11	Q811L3	Q811l3 mus musculu	929	4	66.7	637	16	Q8XUQ7	Q8xug7 ralstonia s
857	4	66.7	567	16	Q8X6D6	Q8x6d6 escherichia	930	4	66.7	637	16	Q8EFF7	Q8eff7 shewanella
858	4	66.7	567	16	Q8ZDN4	Q8zdn4 yersinia pe	931	4	66.7	638	13	Q9I9I4	Q9i9i4 brachydanio
859	4	66.7	570	5	Q9GRS7	Q9grs7 leishmania	932	4	66.7	639	5	Q9GRN8	Q9grn8 leishmania
860	4	66.7	571	11	Q8C636	Q8c636 mus musculu	933	4	66.7	639	15	Q8AGX9	Q8agx9 python molu
861	4	66.7	572	5	Q9GSR0	Q9gsr0 plasmodium	934	4	66.7	639	15	Q8AGX8	Q8agx8 python molu
862	4	66.7	576	2	O87870	O87870 thauera aro	935	4	66.7	640	10	Q9M840	Q9m840 arabidopsis
863	4	66.7	576	2	Q7WSH6	Q7wsh6 comamonas t	936	4	66.7	640	16	Q82TV8	Q82tv8 nitrosomona
864	4	66.7	577	4	Q8IYH3	Q8iyh3 homo sapien	937	4	66.7	641	16	Q81Z62	Q81z62 bacillus an
865	4	66.7	577	10	Q9ATG6	Q9atg6 polytomella	938	4	66.7	641	16	Q81ID5	Q81id5 bacillus ce
866	4	66.7	578	4	Q9NS49	Q9ns49 homo sapien	939	4	66.7	642	5	Q86NU8	Q86nu8 drosophila
867	4	66.7	579	16	Q987F1	Q987f1 rhizobium l	940	4	66.7	642	10	Q84WH9	Q84wh9 arabidopsis
868	4	66.7	583	11	Q8CH93	Q8ch93 rattus norv	941	4	66.7	643	16	Q9HX06	Q9hx06 pseudomonas
869	4	66.7	584	5	Q8MKT8	Q8mkt8 drosophila	942	4	66.7	645	2	Q9FB22	Q9fb22 streptomyce
870	4	66.7	584	16	Q98NT7	Q98nt7 rhizobium l	943	4	66.7	645	6	Q8MJZ5	Q8mjz5 pan troglod
871	4	66.7	584	17	Q8TQM7	Q8tqm7 methanosarc	944	4	66.7	646	10	Q9C792	Q9c792 arabidopsis
872	4	66.7	586	4	Q16526	Q16526 homo sapien	945	4	66.7	649	2	Q84EU9	Q84eu9 methylosinu
873	4	66.7	586	6	Q8WPI9	Q8wpi9 macaca fasc	946	4	66.7	654	16	Q9A6C6	Q9a6c6 caulobacter
874	4	66.7	587	16	Q8ZG34	Q8zg34 yersinia pe	947	4	66.7	654	16	Q8YDS0	Q8yds0 brucella me
875	4	66.7	587	16	Q7UFS3	Q7ufs3 rhodopirell	948	4	66.7	655	13	Q9I9I5	Q9i9i5 brachydanio
876	4	66.7	588	16	Q82G94	Q82g94 streptomyce	949	4	66.7	655	16	Q8YK69	Q8yk69 anabaena sp
877	4	66.7	590	12	Q9Q1V2	Q9qlv2 rabbit pico	950	4	66.7	657	11	Q8R3D4	Q8r3d4 mus musculu
878	4	66.7	590	16	Q89VN6	Q89vn6 bradyrhizob	951	4	66.7	657	16	Q9KB73	Q9kb73 bacillus ha
879	4	66.7	591	16	Q8A2L3	Q8a2l3 bacteroides	952	4	66.7	661	16	Q8FUN0	Q8fun0 brucella su
880	4	66.7	593	2	Q8L1E4	Q8lle4 synechococc	953	4	66.7	662	8	Q7YMD8	Q7ymd8 amischotoly
881	4	66.7	594	13	Q803K2	Q803k2 brachydanio	954	4	66.7	664	10	Q8GXW8	Q8gxw8 arabidopsis
882	4	66.7	596	4	Q9Y6L6	Q9y6l6 homo sapien	955	4	66.7	665	10	Q9MAT2	Q9mat2 arabidopsis
883	4	66.7	598	13	Q9I9I3	Q9i9i3 brachydanio	956	4	66.7	665	16	Q8ZGI4	Q8zgi4 yersinia pe
884	4	66.7	599	16	Q8YHY8	Q8yhy8 brucella me	957	4	66.7	666	4	Q8N8G9	Q8n8g9 homo sapien
885	4	66.7	599	2	O66396	O66396 acinetobact	958	4	66.7	667	11	Q8BTW4	Q8btw4 mus musculu
886	4	66.7	600	2	Q8F864	Q8f864 leptospira	959	4	66.7	669	2	Q56151	Q56151 streptomyce
887	4	66.7	601	16	Q8F864	Q8f864 leptospira	960	4	66.7	670	8	P92280	P92280 congea tome
888	4	66.7	602	16	Q8YYP3	Q8ypy3 anabaena sp	961	4	66.7	675	10	Q7XHM6	Q7xhm6 oryza sativ
889	4	66.7	602	16	Q9S2I8	Q9s2i8 streptomyce	962	4	66.7	678	8	Q33259	Q33259 veronica pa
890	4	66.7	602	16	Q8F426	Q8f426 leptospira	963	4	66.7	678	8	Q85XT5	Q85xt5 panicum val
891	4	66.7	602	16	Q82J57	Q82j57 streptomyce	964	4	66.7	678	16	Q9RYP4	Q9ryp4 deinococcus
892	4	66.7	606	11	P97784	P97784 mus musculu	965	4	66.7	678	16	Q8NNA3	Q8nna3 corynebacte

966 Q8zd61 yersinia pe 66.7 679 16 Q8ZD61
967 Q95gc6 panicum obt 66.7 680 8 Q95GC6
968 Q9sy66 arabidopsis 66.7 680 10 Q9SY66
969 Q95gb6 paspalum co 66.7 682 8 Q95GB6
970 Q95gb5 paspalum we 66.7 683 8 Q95GB5
971 Q95gb7 paspalum re 66.7 683 8 Q95GB7
972 Q95gc0 paspalum va 66.7 683 8 Q95GC0
973 Q95gc1 paspalum ha 66.7 683 8 Q95GC1
974 Q95gb8 paspalum pa 66.7 683 8 Q95GB8
975 Q95g95 thrasya pet 66.7 683 8 Q95G95
976 Q95gb9 paspalum co 66.7 683 8 Q95GB9
977 Q95gb4 paspalum ma 66.7 683 8 Q95GB4
978 Q9pd83 xylella fas 66.7 683 16 Q9PD83
979 Q87dh4 xylella fas 66.7 683 16 Q87DH4
980 Q918q7 pseudomonas 66.7 687 2 Q918Q7
981 Q95g95 anthaenanti 66.7 688 8 Q95GG5
982 Q85xt6 panicum tue 66.7 689 8 Q85XT6
983 Q95g96 thrasya gla 66.7 690 8 Q95G96
984 Q95gc2 paspalum ar 66.7 691 8 Q95GC2
985 Q8kxd6 actinobacil 66.7 695 2 Q8KXD6
986 Q8zcd5 yersinia pe 66.7 699 16 Q8ZCD5
987 Q8cld1 yersinia pe 66.7 699 16 Q8CLD1
988 Q8thr8 methanosarc 66.7 699 17 Q8THR8
989 P92298 gmelina hys 66.7 700 8 P92298
990 Q8a3i5 bacteroides 66.7 702 16 Q8A3I5
991 Q9fhj0 arabidopsis 66.7 703 10 Q9FHJ0
992 Q9fiso arabidopsis 66.7 703 10 Q9FISO
993 Q8gyg3 arabidopsis 66.7 703 10 Q8GYG3
994 Q8xtk8 ralstonia s 66.7 703 16 Q8XTK8
995 Q8kt79 gamma-prote 66.7 706 2 Q8KT79
996 Q7uqt4 rhodopirell 66.7 706 16 Q7UQT4
997 Q9mvh4 colona scab 66.7 707 8 Q9MVH4
998 P73608 synechocyst 66.7 707 16 P73608
999 Q7z2k9 homo sapien 66.7 708 4 Q7Z2K9
1000 Q9mvg7 grewia bilo 66.7 711 8 Q9MVG7

ALIGNMENTS

RESULT 1
Q9ACR5
ID Q9ACR5 PRELIMINARY; PRT; 205 AA.
AC Q9ACR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCP1.253.
GN SCP1.253.
OS Streptomyces coelicolor.
OG Plasmid SCP1.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL590464; CAC36779.1; --
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.

SQ SEQUENCE 205 AA; 23051 MW; 6602396CFF93F2D9 CRC64;
Query Match 83.3%; Score 5; DB 16; Length 205;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 10 ADWSW 14
RESULT 2
Q8IXK8
ID Q8IXK8 PRELIMINARY; PRT; 227 AA.
AC Q8IXK8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to hypothetical protein BC017335.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040173; AAH40173.1; --
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;
Query Match 83.3%; Score 5; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 113 ADWSW 117

RESULT 3
Q7YGU8
ID Q7YGU8 PRELIMINARY; PRT; 228 AA.
AC Q7YGU8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit II.
OS Sphenodon punctatus (Hatteria) (Tuatara).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
OX NCBI_TaxID=8508;
RN [1]
RP SEQUENCE FROM N.A.
RA Rest J.S., Ast J.C., Austin C.C., Waddell P.J., Tibbetts B.A.,
RA Hay J.M., Mindell D.P.;
RT "Molecular systematics of primary reptilian lineages and the tuatara
mitochondrial genome.";
RL Mol. Phylogenet. Evol. 0:0-0(2003).
DR EMBL; AF534390; AAP42708.1; --
KW Mitochondrion.
SQ SEQUENCE 228 AA; 25903 MW; AC52448F76C9F0A4 CRC64;

Query Match 83.3%; Score 5; DB 8; Length 228;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSWA 6
Db 221 DWSWA 225

RESULT 4
Q8NJY9
ID Q8NJY9 PRELIMINARY; PRT; 236 AA.
AC Q8NJY9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endoglucanase.
GN CEL12C.
OS Bionectria ochroleuca (Gliocladium roseum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
OX NCBI_TaxID=29856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22067395; PubMed=12073090;
RA Goedegebuur F., Fowler T., Phillips J., van der Kley P.,
RA van Solingen P., Dankmeyer L., Power S.D.;
RT "Cloning and relational analysis of 15 novel fungal endoglucanases
RT from family 12 glycosyl hydrolase.";
RL Curr. Genet. 41:89-98(2002).
DR EMBL; AF435065; AAM77708.1; -.
DR GO; GO:0008810; P:cellulase activity; IEA.
DR GO; GO:000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR002594; Glyco_hydro_12.
DR Pfam; PF01670; Glyco_hydro_12; 1.
DR ProDom; PD004316; Glyco_hydro_12; 1.
SQ SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;

Query Match 83.3%; Score 5; DB 3; Length 236;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 63 ADWSW 67

RESULT 5
Q919K8
ID Q919K8 PRELIMINARY; PRT; 242 AA.
AC Q919K8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CUN068 hypothetical protein.
GN CUN068.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_TaxID=130556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RX MEDLINE=21488685; PubMed=11602755;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";
RL J. Virol. 75:11157-11165(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF403738; AAK94146.1; -.
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 83.3%; Score 5; DB 12; Length 242;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 80 DWSWA 84

RESULT 6
Q8G659
ID Q8G659 PRELIMINARY; PRT; 274 AA.
AC Q8G659;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable dihydroorotate dehydrogenase electron transfer subunit.
GN PYRK OR BL0790.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaehlen M.-C., Desiere F., Bork P., Delley M.,
RA Fridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014701; AAN24605.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR008333; FAD_binding_6.
DR Pfam; PF00970; FAD_binding_6; 1.
KW Complete proteome.
SQ SEQUENCE 274 AA; 29978 MW; 971E0016E79636DB CRC64;

Query Match 83.3%; Score 5; DB 16; Length 274;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 171 ADWSW 175

RESULT 7
Q8BIT9
ID Q8BIT9 PRELIMINARY; PRT; 355 AA.
AC Q8BIT9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
GN 2810443J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK087998; BAC40084.1; -.
DR MGD; MGI:1914478; 2810443J12Rik.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.

DR	PROSITE; PS00678; WD REPEATS 1; 1.				
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.				
SQ	SEQUENCE 355 AA; 40183 MW; FEF8546127402D58 CRC64;				
Query Match 83.3%; Score 5; DB 11; Length 355;					
Best Local Similarity 100.0%; Pred. No. 72;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 ADWSW 5				
Db	215 ADWSW 219				
RESULT 8					
O50002					
ID	O50002 PRELIMINARY; PRT; 358 AA.				
AC	O50002;				
DT	01-JUN-1998 (TrEMBLrel. 06, Created)				
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Cysteine protease.				
OS	Prunus armeniaca (Apricot).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	euroside 1; Rosales; Rosaceae; Amygdaloideae; Prunus.				
OX	NCBI_TaxID=36596;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Bergeron; TISSUE=Mesocarp, and Exocarp;				
RA	Mbeguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;				
RT	"Sequence of AFTP1, a Cysteine Proteinase From Apricot Fruit				
RT	(Accession No. U93166) . Gene Expression During Fruit Ripening. (PGR97-				
RT	179).";				
RL	Plant Physiol. 115:1730-1730(1997).				
DR	EMBL; U93166; AAB97142.1; -.				
DR	HSSP; P07711; 1CJL.				
DR	MEROPS; C01.041; -.				
DR	GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001092; HLH basic.				
DR	InterPro; IPR000668; Peptidase C1.				
DR	InterPro; IPR000169; SHprot_acsite.				
DR	Pfam; PF00112; Peptidase C1; 1.				
DR	PRINTS; PR00705; PAPAIN.				
DR	ProDom; PD000158; Peptidase C1; 1.				
DR	SMART; SM00645; Pept_C1; 1.				
DR	PROSITE; PS00038; HLH 1; 1.				
DR	PROSITE; PS00640; TH1OL_PROTEASE ASN; 1.				
DR	PROSITE; PS00139; TH1OL_PROTEASE CYS; 1.				
DR	PROSITE; PS00639; TH1OL_PROTEASE_HIS; 1.				
KW	Hydrolase; Protease; Thiol protease.				
SQ	SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;				
Query Match 83.3%; Score 5; DB 10; Length 358;					
Best Local Similarity 100.0%; Pred. No. 73;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 ADWSW 5				
Db	108 ADWSW 112				
RESULT 9					
Q9HZ10					
ID	Q9HZ10 PRELIMINARY; PRT; 374 AA.				
AC	Q9HZ10;				
DT	01-MAR-2001 (TrEMBLrel. 16, Created)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Hypothetical protein PA3230.				
GN	PA3230.				
OS	Pseudomonas aeruginosa.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;				

OC	Pseudomonadaceae; Pseudomonas.				
OX	NCBI_TaxID=287;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 15692 / PAO1;				
RX	MEDLINE=20437337; PubMed=10984043;				
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,				
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,				
RA	Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,				
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,				
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,				
RA	Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;				
RT	"Complete genome sequence of Pseudomonas aeruginosa PAO1, an				
RT	opportunistic pathogen.";				
RL	Nature 406:959-964(2000).				
DR	EMBL; AE004746; AAG06618.1; -.				
DR	PIR; B83241; B83241.				
DR	InterPro; IPR007434; DUF482.				
DR	Pfam; PF04339; DUF482; 1.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;				
Query Match 83.3%; Score 5; DB 16; Length 374;					
Best Local Similarity 100.0%; Pred. No. 76;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2 DWSWA 6				
Db	81 DWSWA 85				
RESULT 10					
Q86KS0					
ID	Q86KS0 PRELIMINARY; PRT; 375 AA.				
AC	Q86KS0;				
DT	01-JUN-2003 (TrEMBLrel. 24, Created)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Dictyostelium discoideum (Slime mold).				
OC	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.				
OX	NCBI_TaxID=44689;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=AX4;				
RX	MEDLINE=22092622; PubMed=12097910;				
RA	Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,				
RA	Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,				
RA	Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;				
RT	"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";				
RL	Nature 418:79-85(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=AX4;				
RA	Baumgart C.;				
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.				
DR	EMBL; AC115612; AA050929.1; -.				
DR	GO; GO:0003824; F:catalytic activity; IEA.				
DR	GO; GO:0008152; P:metabolism; IEA.				
DR	InterPro; IPR000581; ILVD_EDD_family.				
DR	InterPro; IPR006970; PT.				
DR	Pfam; PF04886; PT; 1.				
DR	PROSITE; PS00886; ILVD_EDD_1; 1.				
KW	Hypothetical protein.				
SQ	SEQUENCE 375 AA; 41862 MW; EC9A1D744C56856E CRC64;				
Query Match 83.3%; Score 5; DB 5; Length 375;					
Best Local Similarity 100.0%; Pred. No. 76;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2 DWSWA 6				
Db	47 DWSWA 51				


```
RESULT 11
Q86KF9 ID Q86KF9 PRELIMINARY; PRT; 426 AA.
AC Q86KF9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Mus musculus (Mouse). DnaJ homolog subfamily B member 5
DE (Heat shock protein Hsp40-3) (Heat shock protein cognate 40)
DE (Hsc40).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115680; AAO51091.1; -.
DR GO; GO:0003773; F:heat shock protein activity; IEA.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DNAJ_1; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
KW Heat shock.
SQ SEQUENCE 426 AA; 48376 MW; EBF9F37295925727 CRC64;
```

```
Query Match 83.3%; Score 5; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 DWSWA 6
Db 127 DWSWA 131
```

```
RESULT 12
Q8P4A1 ID Q8P4A1 PRELIMINARY; PRT; 433 AA.
AC Q8P4A1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid:polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
```

```
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012502; AAM43483.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid:polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;
```

```
Query Match 83.3%; Score 5; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 DWSWA 6
Db 181 DWSWA 185
```

```
RESULT 13
Q8PFV8 ID Q8PFV8 PRELIMINARY; PRT; 438 AA.
AC Q8PFV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cationic amino acid transporter.
GN XAC3864.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities.";
RL Nature 417:459-463(2002).
```

```
DR EMBL; AE012036; AAM38706.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid:polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
```


DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 83.3%; Score 5; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 183 DWSWA 187

RESULT 14
Q96AB7 PRELIMINARY; PRT; 452 AA.
ID Q96AB7;
AC Q96AB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017335; AAHI7335.1; -.
DR EMBL; AK075115; BAC11411.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25E38096733 CRC64;

Query Match 83.3%; Score 5; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 338 ADWSW 342

RESULT 15
Q8MMJ0 PRELIMINARY; PRT; 463 AA.
ID Q8MMJ0;
AC Q8MMJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Major royal jelly protein MRJP2 precursor.
GN MRJP2.
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.

OX NCBI_TaxID=7461;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nurse heads;
RA Sittipraneed S., Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525777; AAM88282.1; -.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal.
FT SIGNAL 1 17 POTENTIAL.
SQ SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;

Query Match 83.3%; Score 5; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 110 DWSWA 114

RESULT 16
Q7TF27 PRELIMINARY; PRT; 470 AA.
ID Q7TF27
AC Q7TF27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neuraminidase.
OS Influenza A virus (A/duck/NY/191255-59/02(H5N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=232442;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/duck/NY/191255-59/02;
RA Lee C.-W., Senne D., Linares J.A., Woolcock P., Stallnecht D.,
RA Spackman E., Swayne D., Suarez D.;
RT "Characterization of recent H5 subtype avian influenza viruses from
RT U.S. poultry.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY300948; AAP57560.1; -.
SQ SEQUENCE 470 AA; 52260 MW; 41470434D8ED1662 CRC64;

Query Match 83.3%; Score 5; DB 12; Length 470;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 17
Q9CYU6 PRELIMINARY; PRT; 477 AA.
ID Q9CYU6
AC Q9CYU6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2810443J12Rik protein (Mitochondrial ribosomal protein L41
DE homolog).
GN 2810443J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK013297; BAB28775.1; -.
DR EMBL; AK078448; BAC37279.1; -.
DR MGD; MGI:1914478; 2810443J12Rik.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS0082; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 477 AA; 53201 MW; 2655573524A4BA9C CRC64;

Query Match 83.3%; Score 5; DB 11; Length 477;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 337 ADWSW 341
|||||

RESULT 18
Q9BTV6
ID Q9BTV6 PRELIMINARY; PRT; 484 AA.
AC Q9BTV6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003123; AAH03123.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 3.

DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS0082; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT NON TER 1
SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7358E CRC64;

Query Match 83.3%; Score 5; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 370 ADWSW 374
|||||

RESULT 19
Q8MSH3
ID Q8MSH3 PRELIMINARY; PRT; 581 AA.
AC Q8MSH3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GH24640p.
GN NINAG OR CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118818; AAM50678.1; -.
DR FlyBase; FBgn0037896; ninaG.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000172; GMC_oxred.
DR InterPro; IPR007867; GMC_oxred_C.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF05199; GMC_oxred_C; 1.
DR Pfam; PF00732; GMC_oxred_N; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
SQ SEQUENCE 581 AA; 63475 MW; A2F13BEB25E496D CRC64;

Query Match 83.3%; Score 5; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 159 DWSWA 163
|||||

RESULT 20
Q9VGP2
ID Q9VGP2 PRELIMINARY; PRT; 597 AA.
AC Q9VGP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG6728 protein.
GN NINAG OR CG6728.
OS Drosophila melanogaster (Fruit fly).

OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Berkeley;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhargava P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of Drosophila melanogaster.";
RL	Science 287:2185-2195(2000).
DR	EMBL; AE003691; AAF54634.1; -.
DR	FlyBase; FBgn0037896; ninaG.
DR	GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR00172; GMC_oxred.
DR	InterPro; IPR007867; GMC_oxred C.
DR	InterPro; IPR000169; SHprot_acsite.
DR	Pfam; PF05199; GMC_oxred C; 1.
DR	Pfam; PF00732; GMC_oxred_N; 1.
DR	PROSITE; PS00624; GMC_OXRED_2; 1.
DR	PROSITE; PS00639; THIO_L PROTEASE_HIS; 1.
SQ	SEQUENCE 597 AA; 65274 MW; 8C4C362AFFA0902A CRC64;
Query Match 83.3%; Score 5; DB 5; Length 597;	
Best Local Similarity 100.0%; Pred. No. 1.2e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2 DWSWA 6
Db	159 DWSWA 163
RESULT 21	
Q82MX2	
ID	Q82MX2 PRELIMINARY; PRT; 605 AA.

AC	Q82MX2;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Putative nitric oxide synthase.
GN	SAV1531.
OS	Streptomyces avermitilis.
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC	Streptomycineae; Streptomycetaceae; Streptomyces.
OX	NCBI_TaxID=33903;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX	MEDLINE=21477403; PubMed=11572948;
RA	Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA	Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA	Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT	"Genome sequence of an industrial microorganism Streptomyces
RT	avermitilis: deducing the ability of producing secondary
RT	metabolites.";
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX	MEDLINE=22608306; PubMed=12692562;
RA	Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA	Sakaki Y., Hattori M., Omura S.;
RT	"Complete genome sequence and comparative analysis of the industrial
RT	microorganism Streptomyces avermitilis.";
RL	Nat. Biotechnol. 21:526-531(2003).
DR	EMBL; AP005027; BAC69241.1; -.
DR	GO; GO:0004517; F:nitric-oxide synthase activity; IEA.
DR	GO; GO:0006809; P:nitric oxide biosynthesis; IEA.
DR	InterPro; IPR004030; NO_synthase.
DR	Pfam; PF02898; NO synthase; 1.
DR	PROSITE; PS60001; NOS; 1.
KW	Complete proteome.
SQ	SEQUENCE 605 AA; 65534 MW; 8208F93B381C1FF5 CRC64;
Query Match 83.3%; Score 5; DB 16; Length 605;	
Best Local Similarity 100.0%; Pred. No. 1.2e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ADWSW 5
Db	556 ADWSW 560
RESULT 22	
Q9AAZ6	
ID	Q9AAZ6 PRELIMINARY; PRT; 889 AA.
AC	Q9AAZ6;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	TonB-dependent receptor.
GN	CC0446.
OS	Caulobacter crescentus.
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC	Caulobacteraceae; Caulobacter.
OX	NCBI_TaxID=155892;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 19089 / CB15;
RX	MEDLINE=21173698; PubMed=11259647;
RA	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA	Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA	Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA	DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA	Kolony J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA	Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA	Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT	"Complete genome sequence of Caulobacter crescentus.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005717; AAK22433.1; -.
DR PIR; E87304; E87304.
DR TIGR; CC0446; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00593; TonB_dep_Rec; 1.
KW Receptor; Complete proteome.
SQ SEQUENCE 889 AA; 95775 MW; 75FCBD7A726A01A5 CRC64;

Query Match 83.3%; Score 5; DB 16; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 618 ADWSW 622

RESULT 23

Q9XGZ2 Q9XGZ2 PRELIMINARY; PRT; 1005 AA.
AC Q9XGZ2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TIN24.22 protein (Putative receptor protein kinase).
GN TIN24.22 OR AT5G25930.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Murray J., Langston Y., Clarke K., Drone K.;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Murray J., Langston Y., Clarke K., Drone K.;
RT "The sequence of A. thaliana Tin24.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]

RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF149413; AAD40144.1; -.
DR EMBL; BT004058; AAO42089.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.

DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 1005 AA; 111963 MW; BB006438CC9541C9 CRC64;

Query Match 83.3%; Score 5; DB 10; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 906 ADWSW 910

RESULT 24

Q9L4X2 Q9L4X2 PRELIMINARY; PRT; 5435 AA.
AC Q9L4X2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NysJ.
GN NYSJ.
OS Streptomyces noursei.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1971;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 11455;
RX MEDLINE=20334850; PubMed=10873841;
RA Brautaset T., Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.R.,
RA Valla S., Zotchev S.B.;
RT "Biosynthesis of the polyene antifungal antibiotic nystatin in
RT Streptomyces noursei ATCC 11455: analysis of the gene cluster and
RT deduction of the biosynthetic pathway.";
RL Chem. Biol. 7:395-403(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF263912; AAF71767.1; -.
DR HSSP; P25715; IMLA.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0004314; F:[acyl-carrier protein] S-malonyltransferase. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac_trans.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR004410; FabD.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR006162; Ppantne_S.
DR InterPro; IPR006163; Pp_bind.
DR Pfam; PF00698; Acyl_transf; 3.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF00109; ketoacyl-synt; 3.
DR Pfam; PF02801; ketoacyl-synt_C; 3.
DR Pfam; PF00550; pp-binding; 3.
DR TIGRFAMS; TIGR00128; fabD; 3.
DR PROSITE; PS50075; ACP_DOMAIN; 3.
DR PROSITE; PS00506; B_KETOACYL_SYNTHASE; 3.

RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuono A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003594; BAB75673.1; --
DR PIR; AG2302; AG2302.
DR InterPro; IPR003756; DUF172.
DR InterPro; IPR006442; Phd fam.
DR Pfam; PF02604; DUF172; 1_fam.
DR TIGRFAMs; TIGR01552; phd fam; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 57 AA; 6335 MW; CBC5DEC16952550F CRC64;

Query Match 66.7%; Score 4; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 41 ADWS 44

RESULT 29
Q7UGI2 PRELIMINARY; PRT; 65 AA.
ID Q7UGI2
AC Q7UGI2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB5207.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294141; CAD78347.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 65 AA; 7409 MW; 34A78BF2B514A7FE CRC64;

Query Match 66.7%; Score 4; DB 16; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 28 ADWS 31

RESULT 30
Q99QG6 PRELIMINARY; PRT; 74 AA.
ID Q99QG6
AC Q99QG6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCP1.348.
GN SCP1.348 AND SCP1.06C.
OS Streptomyces coelicolor.

OG Plasmid SCP1.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL590464; CAC36873.1; --
DR EMBL; AL590463; CAC36528.1; --
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 74 AA; 7940 MW; 48C43E8075052C08 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 32 WSWA 35

RESULT 31
Q862X5 PRELIMINARY; PRT; 76 AA.
ID Q862X5
AC Q862X5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to C10 protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22544902; PubMed=12658628;
RA Ishiwata H., Kateuma S., Kizaki K., Patel O.V., Nakano H.,
RA Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
RA Tsujimoto G., Izaike Y., Todoroki J., Hashizume K.;
RT "Characterization of gene expression profiles in early bovine
RT pregnancy using a custom cDNA microarray.";
RL Mol. Reprod. Dev. 65:9-18(2003).
DR EMBL; AB098775; BAC56311.1; --
FT NON_TER 1
FT NON_TER 76
SQ SEQUENCE 76 AA; 8339 MW; 261DDF331051EAD4 CRC64;

Query Match 66.7%; Score 4; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 27 ADWS 30

RESULT 32
Q7UUN4

ID	Q7UUN4	PRELIMINARY;	PRT;	77 AA.
AC	Q7UUN4;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
GN	RB3190.			
OS	Rhodopirellula baltica.			
OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;			
OC	Planctomycetaceae; Pirellula.			
OX	NCBI_TaxID=117;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1;			
RX	MEDLINE=22735913; PubMed=12835416;			
RA	Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,			
RA	Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,			
RA	Schlesner H., Amann R., Reinhardt R.;			
RT	"Complete genome sequence of the marine planctomycete Pirellula sp.			
RT	strain 1.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).			
DR	EMBL; BX294138; CAD73045.1; --			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 77 AA; 9150 MW; FABC9BA1713CD432 CRC64;			
Query Match 66.7%; Score 4; DB 16; Length 77;				
Best Local Similarity 100.0%; Pred. No. 3.3e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ADWS 4			
Db	68 ADWS 71			
RESULT 33				
Q7UGR5				
ID	Q7UGR5	PRELIMINARY;	PRT;	77 AA.
AC	Q7UGR5;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
GN	RB5062.			
OS	Rhodopirellula baltica.			
OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;			
OC	Planctomycetaceae; Pirellula.			
OX	NCBI_TaxID=117;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1;			
RX	MEDLINE=22735913; PubMed=12835416;			
RA	Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,			
RA	Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,			
RA	Schlesner H., Amann R., Reinhardt R.;			
RT	"Complete genome sequence of the marine planctomycete Pirellula sp.			
RT	strain 1.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).			
DR	EMBL; BX294141; CAD78264.1; --			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 77 AA; 8603 MW; 1463926B0338815C CRC64;			
Query Match 66.7%; Score 4; DB 16; Length 77;				
Best Local Similarity 100.0%; Pred. No. 3.3e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ADWS 4			
Db	14 ADWS 17			
RESULT 34				
Q7V158				
ID	Q7V158	PRELIMINARY;	PRT;	82 AA.

AC	Q7V158;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Conserved hypothetical.			
GN	PM1028.			
OS	Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).			
OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;			
OC	Prochlorococcus.			
OX	NCBI_TaxID=59919;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22825698; PubMed=12917642;			
RA	Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,			
RA	Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,			
RA	Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,			
RA	Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,			
RA	Webb E.A., Zinser E.R., Chisholm S.W.;			
RT	"Genome divergence in two Prochlorococcus ecotypes reflects oceanic			
RT	niche differentiation.";			
RL	Nature 424:1042-1047(2003).			
DR	EMBL; BX572092; CAE19487.1; --			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 82 AA; 9368 MW; DEBC78F79859EDA3 CRC64;			
Query Match 66.7%; Score 4; DB 16; Length 82;				
Best Local Similarity 100.0%; Pred. No. 3.5e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ADWS 4			
Db	22 ADWS 25			
RESULT 35				
Q8FBL8				
ID	Q8FBL8	PRELIMINARY;	PRT;	85 AA.
AC	Q8FBL8;			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Hypothetical protein.			
GN	C4754.			
OS	Escherichia coli O6.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=217992;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=O6:H1 / CFT073 / ATCC 700928;			
RX	MEDLINE=22388234; PubMed=12471157;			
RA	Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,			
RA	Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,			
RA	Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,			
RA	Mobley H.L.T., Donnenberg M.S., Blattner F.R.;			
RT	"Extensive mosaic structure revealed by the complete genome sequence			
RT	of uropathogenic Escherichia coli.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).			
DR	EMBL; AE016769; AAN83187.1; --			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 85 AA; 9675 MW; 47DADB502F570A8B CRC64;			
Query Match 66.7%; Score 4; DB 16; Length 85;				
Best Local Similarity 100.0%; Pred. No. 3.6e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	2 DWSW 5			
Db	20 DWSW 23			
RESULT 36				
Q8HAI2				

ID	Q8HAI2	PRELIMINARY;	PRT;	87 AA.	
AC	Q8HAI2;				
DT	01-MAR-2003 (TrEMBLrel. 23, Created)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	Orf-87.				
GN	ORF-87.				
OS	Salmonella typhimurium bacteriophage ST64T.				
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.				
OX	NCBI_TaxID=173443;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Mmolawa P.T., Thomas C.J., Heuzenroeder M.W.;				
RT	"Sequence of the genome of Salmonella enterica serovar Typhimurium bacteriophage ST64T.";				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY052766; AAL15484.1; -.				
SQ	SEQUENCE 87 AA; 9477 MW; C0284919FB92ADC2 CRC64;				
Query Match	66.7%;	Score 4;	DB 9;	Length 87;	
Best Local Similarity	100.0%;	Pred. No. 3.7e+02;			
Matches	4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 ADWS 4				
Db	59 ADWS 62				
RESULT 37					
Q97SD6					
ID	Q97SD6	PRELIMINARY;	PRT;	88 AA.	
AC	Q97SD6;				
DT	01-OCT-2001 (TrEMBLrel. 18, Created)				
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Hypothetical protein SP0448.				
GN	SP0448.				
OS	Streptococcus pneumoniae.				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_TaxID=1313;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC BAA-334 / TIGR4;				
RX	MEDLINE=21357209; PubMed=11463916;				
RA	Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,				
RA	Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,				
RA	Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,				
RA	Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,				
RA	Holtzapfle E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,				
RA	McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,				
RA	Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,				
RA	Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;				
RT	"Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";				
RL	Science 293:498-506(2001).				
DR	EMBL; AE007356; AAK74609.1; -.				
DR	PIR; H95051; H95051.				
DR	TIGR; SP0448; -.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 88 AA; 10274 MW; 0E3E79C00C7DD2F2 CRC64;				
Query Match	66.7%;	Score 4;	DB 16;	Length 88;	
Best Local Similarity	100.0%;	Pred. No. 3.7e+02;			
Matches	4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 ADWS 4				
Db	18 ADWS 21				
RESULT 38					
Q8CZ62					

ID	Q8CZ62	PRELIMINARY;	PRT;	88 AA.	
AC	Q8CZ62;				
DT	01-MAR-2003 (TrEMBLrel. 23, Created)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Hypothetical protein.				
GN	SPR0404.				
OS	Streptococcus pneumoniae (strain ATCC BAA-255 / R6).				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_TaxID=171101;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21429245; PubMed=11544234;				
RA	Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,				
RA	DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,				
RA	Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,				
RA	LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,				
RA	McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,				
RA	Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,				
RA	Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,				
RA	Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,				
RA	Glass J.I.;				
RT	"Genome of the bacterium Streptococcus pneumoniae strain R6.";				
RL	J. Bacteriol. 183:5709-5717(2001).				
DR	EMBL; AE008420; AAK99208.1; -.				
DR	PIR; D97922; D97922.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 88 AA; 10292 MW; 0E2215B011413435 CRC64;				
Query Match	66.7%;	Score 4;	DB 16;	Length 88;	
Best Local Similarity	100.0%;	Pred. No. 3.7e+02;			
Matches	4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 ADWS 4				
Db	18 ADWS 21				
RESULT 39					
Q9F9Z5					
ID	Q9F9Z5	PRELIMINARY;	PRT;	90 AA.	
AC	Q9F9Z5;				
DT	01-MAR-2001 (TrEMBLrel. 16, Created)				
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Serratia entomophila.				
OG	Plasmid PADAP.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Serratia.				
OX	NCBI_TaxID=42906;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=AlMO2;				
RX	MEDLINE=20416224; PubMed=10960097;				
RA	Hurst M.R., Glare T.R., Jackson T.A., Ronson C.W.;				
RT	"Plasmid-located pathogenicity determinants of Serratia entomophila,				
RT	the causal agent of amber disease of grass grub, show similarity to				
RT	the insecticidal toxins of Photobabidus luminescens.";				
RL	J. Bacteriol. 182:5127-5138(2000).				
DR	EMBL; AF135182; AAG09646.1; -.				
DR	GO; GO:0046821; C:extrachromosomal DNA; IEA.				
DR	InterPro; IPR008473; DUF754.				
DR	Pfam; PF05449; DUF754; 1.				
KW	Hypothetical protein; Plasmid.				
SQ	SEQUENCE 90 AA; 10415 MW; CC3B9A4266B9EAA1 CRC64;				
Query Match	66.7%;	Score 4;	DB 2;	Length 90;	
Best Local Similarity	100.0%;	Pred. No. 3.8e+02;			
Matches	4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 ADWS 4				


```

Db          |||||
            61 ADWS 64

RESULT 40
Q8H6W2      PRELIMINARY;      PRT;      92 AA.
AC Q8H6W2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gag-protease polypeptide-like protein (Fragment).
OS Cicer arietinum (Chickpea) (Garbanzo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
OX NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. ICC4958;
RA Benko-Iseppon A.M.; Winter P., Huettel B., Kahl G., Stagginus C.,
RA Muehlbauer F.;
RT "Fine Mapping of Fusarium Resistance in Chickpea (Cicer arietinum L.)
RT using DAF (DNA Amplification Fingerprinting).";
RL Theor. Appl. Genet. 0:0-0(2003).
DR EMBL; AF457593; AAN06609.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
KW Polypeptide; Protease.
FT NON_TER 1 1
FT NON_TER 92 92
SQ SEQUENCE 92 AA; 10030 MW; 98AC81FAF2A958D5 CRC64;

Query Match      66.7%; Score 4; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 ADWS 4
            |||||
Db          68 ADWS 71

RESULT 41
Q939G8      PRELIMINARY;      PRT;      93 AA.
ID Q939G8;
AC Q939G8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ypar4.
OS Pseudomonas alcaligenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=43263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 55044; TRANSPOSON=In55044;
RA Vaisvila R., Morgan R.D., Posfai J., Raleigh E.A.;
RT "Discovery and Distribution of Super-Integrans among Pseudomonads.";
RL Mol. Microbiol. 0:0-0(2001).
DR EMBL; AY038186; AAK73290.1; -.
SQ SEQUENCE 93 AA; 10221 MW; 510C511AB8065D5D CRC64;

Query Match      66.7%; Score 4; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 ADWS 4
            |||||
Db          64 ADWS 67

RESULT 42
Q39643

```


Db					67	ADWS	70
RESULT 44							
Q7U4Q9							
ID	Q7U4Q9	PRELIMINARY;	PRT;	96	AA.		
AC	Q7U4Q9;						
DT	01-OCT-2003	(TReMBLrel. 25, Created)					
DT	01-OCT-2003	(TReMBLrel. 25, Last sequence update)					
DT	01-OCT-2003	(TReMBLrel. 25, Last annotation update)					
DE	Hypothetical.						
GN	SYNW2005.						
OS	Synecococcus sp. (strain WH8102).						
OC	Bacteria; Cyanobacteria; Chroococcales; Synecococcus.						
OX	NCBI_TaxID=84588;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=22825697; PubMed=12917641;						
RA	Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,						
RA	Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,						
RA	Dufresne A., Partensky F., Webb E.A., Waterbury J.;						
RT	"The genome of a motile marine Synecococcus.";						
RL	Nature 424:1037-1042(2003).						
DR	EMBL; BX569694; CAE08520.1; --						
KW	Hypothetical protein; Complete proteome.						
SQ	SEQUENCE 96 AA; 10936 MW; 1C752C8175DFEC45 CRC64;						
Query Match 66.7%; Score 4; DB 16; Length 96;							
Best Local Similarity 100.0%; Pred. No. 4e+02;							
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	3	WSWA	6				
Db	78	WSWA	81				
RESULT 45							
Q8AAB6							
ID	Q8AAB6	PRELIMINARY;	PRT;	98	AA.		
AC	Q8AAB6;						
DT	01-JUN-2003	(TReMBLrel. 24, Created)					
DT	01-JUN-2003	(TReMBLrel. 24, Last sequence update)					
DT	01-OCT-2003	(TReMBLrel. 25, Last annotation update)					
DE	Putative thioredoxin.						
GN	BT0549.						
OS	Bacteroides thetaiotaomicron.						
OC	Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;						
OC	Bacteroidaceae; Bacteroides.						
OX	NCBI_TaxID=818;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=VPI-5482 / ATCC 29148;						
RX	MEDLINE=22550858; PubMed=12663928;						
RA	Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,						
RA	Chiang H.C., Hooper L.V., Gordon J.I.;						
RT	"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";						
RL	Science 299:2074-2076(2003).						
DR	EMBL; AE016928; AAO75656.1; --						
DR	GO; GO:0005489; F:electron transporter activity; IEA.						
DR	GO; GO:0006118; P:electron transport; IEA.						
DR	InterPro; IPR006663; ThioRedox_dom2.						
KW	Complete proteome.						
SQ	SEQUENCE 98 AA; 11466 MW; 133C672116BB881C CRC64;						
Query Match 66.7%; Score 4; DB 16; Length 98;							
Best Local Similarity 100.0%; Pred. No. 4.1e+02;							
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
QY	1	ADWS	4				
Db	23	ADWS	26				

RESULT 46				
Q9JR16				
ID	Q9JR16	PRELIMINARY;	PRT;	100 AA.
AC	Q9JR16;			
DT	01-OCT-2000 (TReMBLrel. 15, Created)			
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)			
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)			
DE	Hypothetical protein NMA0684.			
GN	NMA0684 OR NMB1782.			
OS	Neisseria meningitidis (serogroup A),			
OS	Neisseria meningitidis (serogroup B), and			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=65699, 491, 487;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Z2491 / Serogroup A / Serotype 4A;			
RX	MEDLINE=20222556; PubMed=10761919;			
RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,			
RA	Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,			
RA	Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,			
RA	Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,			
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,			
RA	Whitehead S., Spratt B.G., Barrell B.G.;			
RT	"Complete DNA sequence of a serogroup A strain of Neisseria			
RT	meningitidis Z2491.";			
RL	Nature 404:502-506(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / Serogroup B;			
RX	MEDLINE=20175755; PubMed=10710307;			
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,			
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,			
RA	Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,			
RA	Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,			
RA	Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,			
RA	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,			
RA	Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,			
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;			
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain			
RT	MC58.";			
RL	Science 287:1809-1815(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Z2491 / Serogroup A / Serotype 4A, AND FAM18;			
RX	MEDLINE=20187481; PubMed=10722605;			
RA	Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,			
RA	Tinsley C.R.;			
RT	"Molecular and biological analysis of eight genetic islands that			
RT	distinguish neisseria meningitidis from the closely related pathogen			
RT	neisseria gonorrhoeae.";			
RL	Infect. Immun. 68:2082-2095(2000).			
DR	EMBL; AL162753; CAB83970.1; -.			
DR	EMBL; AE002528; AAF42122.1; -.			
DR	EMBL; AJ391255; CAB71942.1; -.			
DR	EMBL; AJ391284; CAB72071.1; -.			
DR	PIR; H81042; H81042.			
DR	TIGR; NMB1782; -.			
KW	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 100 AA; 10887 MW; 7D87B18A310BE9C3 CRC64;			
Query Match 66.7%; Score 4; DB 16; Length 100;				
Best Local Similarity 100.0%; Pred. No. 4.2e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps				
QY	2	DWSW	5	
Db	77	DWSW	80	
RESULT 47				

Q82UA8	PRELIMINARY;	PRT;	100 AA.
ID Q82UA8;			
AC Q82UA8;			
DT 01-JUN-2003 (TrEMBLrel. 24, Created)			
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE Hypothetical protein.			
GN NE1588.			
OS Nitrosomonas europaea.			
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;			
OC Nitrosomonadaceae; Nitrosomonas.			
OX NCBI_TaxID=915;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=ATCC 19718 / IF0 14298;			
RX MEDLINE=22586410; PubMed=12700255;			
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,			
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,			
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;			
RA "Complete genome sequence of the ammonia-oxidizing bacterium and			
RT obligate chemolithoautotroph Nitrosomonas europaea.";			
RL J. Bacteriol. 185:2759-2773(2003).			
DR EMBL; BX321861; CAD85499.1; -.			
KW Hypothetical protein; Complete proteome.			
SQ SEQUENCE 100 AA; 11563 MW; A067551AA5350CD0 CRC64;			
Query Match 66.7%; Score 4; DB 16; Length 100;			
Best Local Similarity 100.0%; Pred. No. 4.2e+02;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 ADWS 4			
Db 36 ADWS 39			
RESULT 48			
Q8GSE6	PRELIMINARY;	PRT;	101 AA.
ID Q8GSE6			
AC Q8GSE6;			
DT 01-MAR-2003 (TrEMBLrel. 23, Created)			
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE P0438G07.16 protein (B1126F07.16 protein).			
GN P0438G07.16 OR B1126F07.16.			
OS Oryza sativa (japonica cultivar-group).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC Ehrhartoideae; Oryzeae; Oryza.			
OX NCBI_TaxID=39947;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=cv. Nipponbare;			
RA Sasaki T., Matsumoto T., Yamamoto K.;			
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC			
clone:P0438G07.";			
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RC STRAIN=cv. Nipponbare;			
RA Sasaki T., Matsumoto T., Katayose Y.;			
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC			
clone:B1126F07.";			
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AP004398; BAC22373.1; -.			
DR EMBL; AP005674; BAC22484.1; -.			
SQ SEQUENCE 101 AA; 10894 MW; 2C12C798D110A081 CRC64;			
Query Match 66.7%; Score 4; DB 10; Length 101;			
Best Local Similarity 100.0%; Pred. No. 4.2e+02;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 ADWS 4			
Db 36 ADWS 39			

Db	35 ADWS 38
RESULT 49	
Q7V3S8	PRELIMINARY;
ID Q7V3S8	PRT; 101 AA.
AC Q7V3S8;	
DT 01-OCT-2003 (TrEMBLrel. 25, Created)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE Hypothetical protein.	
GN PMT2263.	
OS Prochlorococcus marinus (strain MIT 9313).	
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;	
OC Prochlorococcus.	
OX NCBI_TaxID=74547;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=22825698; PubMed=12917642;	
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,	
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,	
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,	
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,	
RA Webb E.A., Zinser E.R., Chisholm S.W.;	
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic	
niche differentiation.";	
RL Nature 424:1042-1047(2003).	
DR EMBL; BX572101; CAE22437.1; -.	
KW Hypothetical protein; Complete proteome.	
SQ SEQUENCE 101 AA; 11390 MW; 4518CBD4F8955AEA CRC64;	
Query Match 66.7%; Score 4; DB 16; Length 101;	
Best Local Similarity 100.0%; Pred. No. 4.2e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 ADWS 4	
Db 3 ADWS 6	
RESULT 50	
Q68355	PRELIMINARY;
ID Q68355	PRT; 103 AA.
AC Q68355;	
DT 01-NOV-1996 (TrEMBLrel. 01, Created)	
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE Core protein (Genome polypeptide) (Fragment).	
GN C.	
OS Hepatitis C virus.	
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	
OC Hepacivirus.	
OX NCBI_TaxID=11103;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=EUPK22;	
RA Mellor J., Holmes E.C., Jarvis L.M., Yap P.L., Simmonds P.,	
RA International Collaborators;	
RT "Investigation of the pattern of hepatitis C virus sequence diversity	
in different geographical regions: implications for virus	
classification.";	
RL J. Gen. Virol. 0:0-0(1995).	
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A	
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:	
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF	
CC PROTEIN C AND MRNA (BY SIMILARITY).	
DR EMBL; U31251; AAA75055.1; -.	
DR GO; GO:0019028; C:viral capsid; IEA.	
DR GO; GO:0005198; F:structural molecule activity; IEA.	
DR InterPro; IPR002522; HCV capsid.	
DR Pfam; PF01543; HCV_capsid; 1.	
KW Polyprotein.	
FT NON_TER 1 1	

FT NON TER 103 103
SQ SEQUENCE 103 AA; 11690 MW; 0534281AAAC29CA4 CRC64;
Query Match 66.7%; Score 4; DB 12; Length 103;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 WSWA 6
Db 65 WSWA 68

Search completed: July 23, 2004, 13:26:12
Job time : 64 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:21:20 ; Search time 14 Seconds
(without alignments)
22.316 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 6

Sequence: 1 ADWSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	83.3	470	1	NRAM_IADBU Q07570 influenza a
2	5	83.3	470	1	NRAM_IADCH Q07571 influenza a
3	5	83.3	470	1	NRAM_IADH2 Q07572 influenza a
4	5	83.3	470	1	NRAM_IADM2 Q07573 influenza a
5	5	83.3	470	1	NRAM_IADU3 Q07599 influenza a
6	5	83.3	470	1	NRAM_IAGFN Q07574 influenza a
7	5	83.3	470	1	NRAM_IAHGD Q07577 influenza a
8	5	83.3	470	1	NRAM_IAHJI Q07578 influenza a
9	5	83.3	470	1	NRAM_IAMAE Q07583 influenza a
10	5	83.3	470	1	NRAM_IATKL Q07585 influenza a
11	5	83.3	598	1	MRJ5_APIME Q97432 apis mellif
12	4	66.7	31	1	LCCB_LEUME P81052 leuconostoc
13	4	66.7	36	1	TXD3_PARLU P83258 paracoelote
14	4	66.7	37	1	TXD1_PARLU P83256 paracoelote
15	4	66.7	93	1	ACYP_MYCTU P56543 mycobacteri
16	4	66.7	114	1	Y451_BUCAP Q8k998 buchnera ap
17	4	66.7	128	1	YRDN_BACSU P94502 bacillus su
18	4	66.7	147	1	VG29_BPMD2 O64223 mycobacteri
19	4	66.7	147	1	VG29_BPML5 Q05236 mycobacteri
20	4	66.7	160	1	YB19_PSEPK Q88nt5 pseudomonas
21	4	66.7	169	1	CX41_MOUSE P19783 mus musculu
22	4	66.7	169	1	CX41_RAT P10888 rattus norv
23	4	66.7	182	1	RL18_HALN1 P50562 halobacteri
24	4	66.7	197	1	YE21_AQUAE O67415 aquifex aeo
25	4	66.7	200	1	HAM1_STRPN Q97nx3 streptococc
26	4	66.7	208	1	TATB_XANAC Q8pex3 xanthomonas
27	4	66.7	213	1	VNCN_PAVBO P07295 bovine parv
28	4	66.7	227	1	RECO_PSESM Q87xg3 pseudomonas
29	4	66.7	233	1	RECO_PSEAE Q9xcx7 pseudomonas
30	4	66.7	237	1	UBIE_LISMO Q92a77 listeria mo
31	4	66.7	256	1	TAM_RHILO Q98k73 rhizobium l
32	4	66.7	257	1	YK09_RALSO Q8xxv4 ralstonia s
33	4	66.7	262	1	DET2_ARATH Q38944 arabidopsis

34	4	66.7	272	1	CY1_RHORU P23135 rhodospiril
35	4	66.7	279	1	HRP5_HUMAN Q96kn8 homo sapien
36	4	66.7	280	1	CHR2_PSEAE Q916v7 pseudomonas
37	4	66.7	282	1	3MG2_ECOLI P04395 escherichia
38	4	66.7	284	1	RP32_PSEAE P42378 pseudomonas
39	4	66.7	289	1	PORI_RHOB L P39767 rhodopsendo
40	4	66.7	291	1	C552_PSEST P24037 pseudomonas
41	4	66.7	295	1	RSP4_BOVIN P26452 bos taurus
42	4	66.7	295	1	RSP4_CRIGR P38982 cricetus
43	4	66.7	295	1	RSP4_HUMAN P08865 homo sapien
44	4	66.7	295	1	RSP4_MOUSE P14206 mus musculu
45	4	66.7	295	1	RSP4_RAT P38983 rattus norv
46	4	66.7	296	1	RSP4_CHICK P50890 gallus gall
47	4	66.7	302	1	DHMA_CAUCR Q9a919 caulobacter
48	4	66.7	304	1	NXP4_RAT Q922n4 rattus norv
49	4	66.7	307	1	CRTE_ERWHE P23873 erwinia her
50	4	66.7	308	1	NXP4_HUMAN O95158 homo sapien
51	4	66.7	319	1	FMT_TREPA O83737 treponema p
52	4	66.7	328	1	DUS_AZOB R P45672 azospirillu
53	4	66.7	331	1	LAD2_ENTFA Q833w8 enterococcu
54	4	66.7	332	1	DUSA_XYLFT Q87ay2 xylella fas
55	4	66.7	340	1	DUSA_XYLFA Q9pgb5 xylella fas
56	4	66.7	346	1	PSTS_ECOLI P06128 escherichia
57	4	66.7	347	1	HEMZ_CAUCR P57777 caulobacter
58	4	66.7	347	1	OXDA_HUMAN P14920 homo sapien
59	4	66.7	347	1	OXDA_RABIT P22942 oryctolagus
60	4	66.7	348	1	GTOM_ARATH Q9zsk1 arabidopsis
61	4	66.7	351	1	DESA_SVNY3 P20388 synechocyst
62	4	66.7	354	1	ALKB_ARATH Q9aa98 arabidopsis
63	4	66.7	360	1	WNT2_CAEEL P34889 caenorhabdi
64	4	66.7	361	1	YB19_SVNY3 P73341 synechocyst
65	4	66.7	362	1	DCUP_YEAST P32347 saccharomyc
66	4	66.7	363	1	PSPB_CANFA P17129 canis famil
67	4	66.7	364	1	PSTS_XYLFA Q9pbk3 xylella fas
68	4	66.7	364	1	PSTS_XYLFT Q87c91 xylella fas
69	4	66.7	375	1	PEX7_YEAST P39108 saccharomyc
70	4	66.7	376	1	PGLR_PENGR O93883 penicillium
71	4	66.7	390	1	Y378_HALN1 Q9hs70 halobacteri
72	4	66.7	394	1	PGK_BACST P18912 bacillus st
73	4	66.7	394	1	TGT_DEIRA Q9rrb5 deinococcus
74	4	66.7	399	1	PDK_ASCSU O02623 ascaris suu
75	4	66.7	401	1	BMP4_XENLA P30885 xenopus lae
76	4	66.7	401	1	PDK_CAEEL Q02332 caenorhabdi
77	4	66.7	409	1	AXIA_BRARE Q07342 brachydanio
78	4	66.7	411	1	FOLC_BUCAI P57265 buchnera ap
79	4	66.7	413	1	YTH1_PANTH P46351 paenibacill
80	4	66.7	416	1	YTH16_CHICK P18519 gallus gall
81	4	66.7	437	1	YTH3_RHOER P46372 rhodococcus
82	4	66.7	439	1	TSAT_TAXCH Q8e996 taxus chine
83	4	66.7	439	1	T5AT_TAXCU Q9m6f0 taxus cuspi
84	4	66.7	445	1	YKAB_BACPF P30268 bacillus ps
85	4	66.7	452	1	CBL1_ARATH Q9ert7 arabidopsis
86	4	66.7	453	1	NRAM_IAWIL P03470 influenza a
87	4	66.7	454	1	NRAM_IAPUE P03468 influenza a
88	4	66.7	460	1	HEMN_PSEAE P77915 pseudomonas
89	4	66.7	467	1	MURD_BRUME Q8yi68 brucella me
90	4	66.7	467	1	MURD_BRUSU Q8fzp2 brucella su
91	4	66.7	471	1	MANC_KLEPN Q48462 klebsiella
92	4	66.7	471	1	MURD_CAUCR Q9a597 caulobacter
93	4	66.7	471	1	RFM9_ECOLI P37753 escherichia
94	4	66.7	474	1	CBF5_SCHPO O14007 schizosacch
95	4	66.7	477	1	YZ64_SVNY3 P73436 synechocyst
96	4	66.7	483	1	LIA2_HUMAN Q8nl49 homo sapien
97	4	66.7	484	1	SGAT_ECOLI P39301 escherichia
98	4	66.7	487	1	YK75_MYCTU Q10683 mycobacteri
99	4	66.7	488	1	PAC2_RAT Q9qy17 rattus norv
100	4	66.7	491	1	G6PD_BUCAI P57405 buchnera ap
101	4	66.7	501	1	GUAA_THEME Q9x2e0 thermotoga
102	4	66.7	501	1	PLI3_ARATH Q93z04 arabidopsis
103	4	66.7	505	1	GUAA_PYRAB Q8zt92 pyrobaculum
104	4	66.7	526	1	GUAA_STRCO Q910h2 streptomyc
105	4	66.7	547	1	OM6C_CHLTR P26758 chlamydia t
106	4	66.7	547	1	OM6D_CHLTR P18151 chlamydia t

107	4	66.7	547	1	OM6E_CHLTR	P23603	chlamydia t	180	4	66.7	1107	1	POL2_RRVS	P36324	raspberry r
108	4	66.7	547	1	OM6L_CHLTR	P21354	chlamydia t	181	4	66.7	1125	1	YE62_SCHPO	O14248	schizosacch
109	4	66.7	550	1	VGLE_HSV11	P04488	herpes simp	182	4	66.7	1230	1	UGS4_SOLTU	Q43846	solanum tub
110	4	66.7	552	1	GPMI_LEPIN	P59173	leptospira	183	4	66.7	1259	1	YTFN_ECOLI	P39321	escherichia
111	4	66.7	556	1	OM6_CHLPN	P23700	chlamydia p	184	4	66.7	1331	1	MANB_CALSA	P22533	caldocellum
112	4	66.7	557	1	OM6_CHLPS	P23701	chlamydia p	185	4	66.7	1423	1	FRUA_STRMU	Q03174	streptococc
113	4	66.7	567	1	IF37_SCHPO	Q94236	schizosacch	186	4	66.7	1573	1	ARO1_SCHPO	Q9p7r0	s pentafunc
114	4	66.7	570	1	DFAS_ANASP	Q820c1	anabaena sp	187	4	66.7	1616	1	RRPO_TMOB	P90211	tobamovirus
115	4	66.7	578	1	HAS1_HUMAN	Q92839	homo sapien	188	4	66.7	1742	1	GUNA_CALSA	P22534	caldocellum
116	4	66.7	579	1	YC12_KLEPN	Q48458	klebsiella	189	4	66.7	1978	1	MYHB_CHICK	P10587	gallus gall
117	4	66.7	583	1	HAS1_MOUSE	Q61647	mus musculus	190	4	66.7	3175	1	RPOA_EAV	P19811	equine arte
118	4	66.7	597	1	PEPX_BACAA	Q81pe9	bacillus an	191	4	66.7	3421	1	TEGU_HSVBB	P28955	equine herp
119	4	66.7	601	1	DNJM_MYCGE	P47442	mycoplasma	192	4	66.7	6684	1	RIAB_CVPPU	Q91w06	p replicase
120	4	66.7	605	1	PHAC_METEX	P52070	methylobact	193	3	50.0	10	1	AKHX_LOCMI	P81626	locusta mig
121	4	66.7	608	1	UL27_HCMVA	P16763	human cytom	194	3	50.0	14	1	MAST_VESBA	P21654	vespa basal
122	4	66.7	626	1	SAD1_HUMAN	Q9y3z3	homo sapien	195	3	50.0	27	1	PSBY_FUCVE	Q9bac7	fucus vesic
123	4	66.7	630	1	Y242_MYCGE	P47484	mycoplasma	196	3	50.0	32	1	PSBZ_EUGVI	Q8e187	euglena vir
124	4	66.7	648	1	AMO1_ARTS1	Q07121	arthrobacte	197	3	50.0	35	1	PSBY_CYAME	Q85961	cyanidiosch
125	4	66.7	648	1	AMO2_ARTS1	Q07123	arthrobacte	198	3	50.0	36	1	PSBY_ODOSI	P49543	odontella s
126	4	66.7	671	1	Z282_HUMAN	Q9udv7	homo sapien	199	3	50.0	36	1	PSBY_PORPU	P51206	porphyra pu
127	4	66.7	675	1	NED1_MOUSE	P33215	mus musculus	200	3	50.0	37	1	PSBY_CYACA	O19893	cyanidium c
128	4	66.7	689	1	MEA_ATH	O65312	arabidopsis	201	3	50.0	37	1	PSBY_GUITH	O78433	guillardia
129	4	66.7	692	1	YK06_YEAST	P36062	saccharomyc	202	3	50.0	37	1	TXD4_PARLU	P83259	paracoelete
130	4	66.7	698	1	TR85_YEAST	P46944	saccharomyc	203	3	50.0	37	1	TXM2_AGEAP	P11058	agelenopsis
131	4	66.7	700	1	GUNA_PAEAL	P29719	paenibacill	204	3	50.0	37	1	TXM4_AGEAP	P11060	agelenopsis
132	4	66.7	702	1	DY12_ANTCR	Q16959	anthocidari	205	3	50.0	37	1	TXM5_AGEAP	P11061	agelenopsis
133	4	66.7	705	1	GUN6_DICDI	P22699	dictyosteli	206	3	50.0	37	1	TXM6_AGEAP	P11062	agelenopsis
134	4	66.7	715	1	ZP2_CANFA	P47983	canis famil	207	3	50.0	38	1	TXC2_HOLCU	P60177	hololena cu
135	4	66.7	716	1	ZP2_FELCA	P47984	felis silve	208	3	50.0	38	1	TXC3_HOLCU	P15968	hololena cu
136	4	66.7	720	1	FPTA_PSEAE	P42512	pseudomonas	209	3	50.0	38	1	TXM3_AGEAP	P60178	agelenopsis
137	4	66.7	730	1	CATR_ASPNG	P55303	aspergillus	210	3	50.0	40	1	ALF_CANAL	Q9urb4	candida alb
138	4	66.7	739	1	GUNF_CLOTM	P26224	clostridium	211	3	50.0	40	1	YC04_ARCFU	O29064	archaeoglob
139	4	66.7	743	1	PURL_RHILO	Q98nn7	rhizobium l	212	3	50.0	43	1	PSBY_SYNPK	P59908	synecococc
140	4	66.7	745	1	IKKA_HUMAN	O15111	h inhibitor	213	3	50.0	44	1	PISI_CARPI	P80569	carnobacter
141	4	66.7	745	1	IKKA_MOUSE	Q60680	m inhibitor	214	3	50.0	45	1	ATI2_HSVE4	Q00041	equine herp
142	4	66.7	756	1	IKKB_HUMAN	O14920	homo sapien	215	3	50.0	49	1	LYC_PSEPE	P21776	pseudocheir
143	4	66.7	757	1	IKKB_MOUSE	O88351	mus musculus	216	3	50.0	52	1	RUBR_DESVH	P00269	desulfovibr
144	4	66.7	757	1	IKKB_RAT	Q9gy78	rattus norv	217	3	50.0	52	1	RUBR_HELMO	P15412	desulfovibr
145	4	66.7	757	1	PEPX_STRPN	Q97rc8	streptococc	218	3	50.0	52	1	RUBR_MEGEL	P56263	helioabacill
146	4	66.7	757	1	PEPX_STRR6	Q8dg87	streptococc	219	3	50.0	52	1	RUBR_MEGEL	P00271	megasphaera
147	4	66.7	761	1	PEPX_STRA3	Q8e3h8	streptococc	220	3	50.0	53	1	VG87_BPML5	Q05304	mycobacteri
148	4	66.7	773	1	DHAQ_ACEPO	P17201	acetobacter	221	3	50.0	54	1	B2MG_MESAU	P30442	mesocricetu
149	4	66.7	783	1	PKC7_RAT	Q62849	rattus norv	222	3	50.0	54	1	CH03_CHICK	P40667	gallus gall
150	4	66.7	810	1	YLZ5_CAEEL	P34418	caenorhabdi	223	3	50.0	55	1	ATP8_RHEAM	O64268	mycobacteri
151	4	66.7	813	1	PMAX_ARATH	Q9t0e0	arabidopsis	224	3	50.0	55	1	SOX1_PLEWA	Q79396	rhea americ
152	4	66.7	835	1	SYFB_MYCLE	Q9cc16	mycobacteri	225	3	50.0	56	1	IE12_HSV2	P37839	pleurodeles
153	4	66.7	836	1	GCS1_HUMAN	Q13724	homo sapien	226	3	50.0	58	1	IVBI_DENAN	P00980	dendroaspis
154	4	66.7	862	1	SYV_THETH	P96142	thermus the	227	3	50.0	59	1	SCKD_LEIQH	P45628	leiurus qui
155	4	66.7	891	1	NIA7_HORVU	P27968	hordeum vul	228	3	50.0	59	1	RUB4_RHOER	Q9ae66	rhodococcus
156	4	66.7	895	1	ODP1_ALCEU	Q59097	alcaligenes	229	3	50.0	60	1	YMFR_ECOLI	P75979	escherichia
157	4	66.7	910	1	NUOG_BUCAP	Q8k9y2	buchnera ap	230	3	50.0	60	1	SIX4_BUTSI	P82814	buthus sind
158	4	66.7	911	1	NIA2_BRANA	P39868	brassica na	231	3	50.0	62	1	RUB2_RHOER	Q9ae63	rhodococcus
159	4	66.7	917	1	SYI_CAMJE	P41257	campylobact	232	3	50.0	63	1	YACG_SALTY	Q8xfy1	salmonella
160	4	66.7	929	1	YDM6_SCHPO	P87137	schizosacch	233	3	50.0	64	1	ENPP_BPPA2	P10438	bacterioph
161	4	66.7	944	1	GLND_RHILV	Q9rae4	rhizobium l	234	3	50.0	64	1	YC20_GUITH	O78445	guillardia
162	4	66.7	948	1	GLND_RHITR	Q53245	rhizobium t	235	3	50.0	65	1	VXIS_BPPH8	P05998	bacterioph
163	4	66.7	977	1	UB24_HUMAN	Q9upu5	homo sapien	236	3	50.0	65	1	YACG_ECOL6	Q8fl57	escherichia
164	4	66.7	983	1	EPA3_CHICK	P29318	gallus gall	237	3	50.0	65	1	YACG_ECOLI	P36681	escherichia
165	4	66.7	983	1	EPA3_HUMAN	P29320	homo sapien	238	3	50.0	66	1	UL90_HCMVA	P16796	human cytom
166	4	66.7	983	1	EPA3_MOUSE	P29319	mus musculus	239	3	50.0	67	1	PSBH_ODOSI	P49475	odontella s
167	4	66.7	984	1	EPA3_RAT	O08680	rattus norv	240	3	50.0	69	1	RUB1_CHLTE	P58992	chlorobium
168	4	66.7	994	1	SYV_XYLFA	Q9ph12	xylella fas	241	3	50.0	71	1	NXL1_NAJME	P01383	naja melano
169	4	66.7	994	1	SYV_XYLFT	Q87f36	xylella fas	242	3	50.0	71	1	YE90_HAEIN	P44216	haemophilus
170	4	66.7	1036	1	PLD1_CRIGR	O08684	cricetulus	243	3	50.0	72	1	ATP8_METSE	O47493	metridium s
171	4	66.7	1039	1	GUNB_CALSA	P10474	c endogluca	244	3	50.0	73	1	YVAI_VACCC	P20518	vaccinia vi
172	4	66.7	1039	1	Y4JQ_RHISN	P55517	rhizobium s	245	3	50.0	74	1	SMS2_MYOSC	P09876	myoxocephal
173	4	66.7	1057	1	ANPA_MOUSE	P18293	mus musculus	246	3	50.0	75	1	REGB_PSEAE	Q03381	pseudomonas
174	4	66.7	1057	1	ANPA_RAT	P18910	rattus norv	247	3	50.0	78	1	IAA1_STRGS	P01093	streptomyce
175	4	66.7	1061	1	ANPA_HUMAN	P16066	homo sapien	248	3	50.0	79	1	NU5M_MACFA	P50665	macaca fasc
176	4	66.7	1074	1	PLD1_HUMAN	Q13393	homo sapien	249	3	50.0	80	1	Y14C_BPT4	P39506	bacterioph
177	4	66.7	1074	1	PLD1_MOUSE	Q9z280	mus musculus	250	3	50.0	81	1	HPIS_THIPF	P00263	thiocapsa p
178	4	66.7	1074	1	PLD1_RAT	P70496	rattus norv	251	3	50.0	82	1	HPIS_MARPU	P59860	marichromat
179	4	66.7	1097	1	LIFR_HUMAN	P42702	homo sapien	252	3	50.0					

180	4	66.7	1107	1	POL2_RRVS	P36324	raspberry r
181	4	66.7	1125	1	YE62_SCHPO	O14248	schizosacch
182	4	66.7	1230	1	UGS4_SOLTU	Q43846	solanum tub
183	4	66.7	1259	1	YTFN_ECOLI	P39321	escherichia
184	4	66.7	1331	1	MANB_CALSA	P22533	caldocellum
185	4	66.7	1423	1	FRUA_STRMU	Q03174	streptococ
186	4	66.7	1573	1	ARO1_SCHPO	Q9p7r0	s pentafunc
187	4	66.7	1616	1	RRPO_TMOB	P90211	tobamovirus
188	4	66.7	1742	1	GUNA_CALSA	P22534	caldocellum
189	4	66.7	1978	1	MYHB_CHICK	P10587	gallus gall
190	4	66.7	3175	1	RPOA_EAV	P19811	equine arte
191	4	66.7	3421	1	TEGU_HSVB	P28955	equine herp
192	4	66.7	6684	1	RIAB_CVPPU	Q91w06	p replicase
193	3	50.0	10	1	AKHX_LOCM1	P81626	locusta mig
194	3	50.0	14	1	MAST_VESBA	P21654	vespa basal
195	3	50.0	27	1	PSBY_FUCVE	Q9bac7	fucus vesic
196	3	50.0	32	1	PSBZ_EUGVI	Q8e187	euglena vir
197	3	50.0	35	1	PSBY_CYAME	Q85g61	cyanidiosch
198	3	50.0	36	1	PSBY_ODOSI	P49543	odontella s
199	3	50.0	36	1	PSBY_PORPU	P51206	porphyra pu
200	3	50.0	37	1	PSBY_CYACA	O19893	cyanidium c
201	3	50.0	37	1	PSBY_GUITH	O78433	guillardia
202	3	50.0	37	1	TXD4_PARLU	P83259	paracoelote
203	3	50.0	37	1	TXM2_AGEAP	P11058	agelenopsis
204	3	50.0	37	1	TXM4_AGEAP	P11060	agelenopsis
205	3	50.0	37	1	TXM5_AGEAP	P11061	agelenopsis
206	3	50.0	37	1	TXM6_AGEAP	P11062	agelenopsis
207	3	50.0	38	1	TXC2_HOLCU	P60177	hololena cu
208	3	50.0	38	1	TXC3_HOLCU	P15968	hololena cu
209	3	50.0	38	1	TXM3_AGEAP	P60178	agelenopsis
210	3	50.0	40	1	ALF_CANAL	Q9urb4	candida alb
211	3	50.0	40	1	YC04_ARCFU	O29064	archaeoglob
212	3	50.0	43	1	PSBY_SYNPX	P59908	synechococc
213	3	50.0	44	1	PIS1_CARP1	P80569	carnobacter
214	3	50.0	45	1	AT12_HSVE4	Q00041	equine herp
215	3	50.0	49	1	LYC_PSEPE	P21776	pseudoeheir
216	3	50.0	52	1	RUBR_DESVH	P00269	desulfovibr
217	3	50.0	52	1	RUBR_DESVM	P15412	desulfovibr
218	3	50.0	52	1	RUBR_HELMO	P56263	heliobacill
219	3	50.0	52	1	RUBR_MEGEL	P00271	megasphaera
220	3	50.0	53	1	VG87_BPML5	Q05304	mycobacteri
221	3	50.0	54	1	B2MG_MESAU	P30442	mesocricetu
222	3	50.0	54	1	CH03_CHICK	P40667	gallus gall
223	3	50.0	54	1	VG87_BPMD2	O64268	mycobacteri
224	3	50.0	55	1	ATP8_RHEAM	O79396	rhea americ
225	3	50.0	56	1	SOX1_PLEWA	P37839	pleurodeles
226	3	50.0	58	1	IE12_HSV2	P14345	herpes simp
227	3	50.0	59	1	IVEI_DENAN	P00980	dendroaspis
228	3	50.0	59	1	SCKD_LEIQH	P45628	leiurus qui
229	3	50.0	60	1	RUB4_RHOER	Q9ae66	rhodococcus
230	3	50.0	60	1	YMER_ECOLI	P75979	escherichia
231	3	50.0	62	1	SIX4_BUTSI	P82814	buthus sind
232	3	50.0	63	1	RUB2_RHOER	Q9ae63	rhodococcus
233	3	50.0	63	1	YACG_SALTY	Q8xfy1	salmonella
234	3	50.0	64	1	ENPP_BPPA2	P10438	bacterioph
235	3	50.0	64	1	YC20_GUITH	O78445	guillardia
236	3	50.0	65	1	VXIS_BPPH8	P05998	bacterioph
237	3	50.0	65	1	YACG_ECOLI	Q8fl57	escherichia
238	3	50.0	65	1	YACG_ECOLI	P36681	escherichia
239	3	50.0	66	1	UL90_HCMVA	P16796	human cytom
240	3	50.0	67	1	PSBH_ODOSI	P49475	odontell
241	3	50.0	69	1	RUB1_CHLTE	P58992	chlorobium
242	3	50.0	71	1	NXLI_NAJME	P01383	naja melano
243	3	50.0	71	1	YE90_HAEIN	P44216	haemophilus
244	3	50.0	72	1	ATP8_METSE	O47493	metridium s
245	3	50.0	73	1	YVAI_VACCC	P20518	vaccinia vi
246	3	50.0	74	1	SMS2_MYOSC	P09876	myoxoceph
247	3	50.0	75	1	REGB_PSEAE	Q03381	pseudomonas
248	3	50.0	78	1	IAAL_STRGS	P01093	streptomyce
249	3	50.0	79	1	NUSM_MACFA	P50665	macaca fasc
250	3	50.0	80	1	Y14C_BPT4	P39506	bacterioph
251	3	50.0	81	1	HPIS_THIPF	P00263	thiocapsa p
252	3	50.0	82	1	HPIS_MARPU	P59860	marichromat

253	3	50.0	83	1	YC20_GALSU	P48409	galdieria s	326	3	50.0	108	1	Y095_ARCFU	O30141	archaeoglob
254	3	50.0	84	1	D119_HUMAN	Q8n690	homo sapien	327	3	50.0	108	1	YML2_THIPE	P20088	thiobacillu
255	3	50.0	85	1	YHDT_HAEIN	P46455	haemophilus	328	3	50.0	108	1	YNFA_SALT1	Q8z6z2	salmonella
256	3	50.0	86	1	TRBE_ECOLI	Q05807	escherichia	329	3	50.0	109	1	BPHF_BURCE	P37332	burkholderi
257	3	50.0	88	1	IE12_HSV11	P03170	herpes simp	330	3	50.0	109	1	CYPC_STRHA	Q05368	streptomyce
258	3	50.0	88	1	YQ38_BACHD	P09K97	bacillus ha	331	3	50.0	109	1	KV4D_HUMAN	P83593	homo sapien
259	3	50.0	89	1	VAP1_RIEAN	Q85172	riemerella	332	3	50.0	110	1	UVRA_PARDE	P29927	paracoccu
260	3	50.0	89	1	Y4MD_RHISN	P55563	rhizobium s	333	3	50.0	110	1	YCT1_YEAST	P37265	saccharomyc
261	3	50.0	89	1	YNAX_KLEAE	Q08600	klebsiella	334	3	50.0	111	1	CYC6_ANASP	P28596	anabaena sp
262	3	50.0	90	1	VP9_BPPH6	P07581	bacterioph	335	3	50.0	111	1	CYC_ENTIN	P00075	enteromorph
263	3	50.0	90	1	Y285_PSEPK	Q88r49	pseudomonas	336	3	50.0	111	1	VPX_HV2D2	P15836	human immun
264	3	50.0	90	1	YFIM_ECOLI	P46126	escherichia	337	3	50.0	111	1	Y161_UREPA	Q9pgy3	ureaplasma
265	3	50.0	90	1	YHE3_PSESM	Q87uf5	pseudomonas	338	3	50.0	111	1	YGN2_YEAST	P53126	saccharomyc
266	3	50.0	91	1	LCIB_LACLC	P35517	lactococcus	339	3	50.0	112	1	CFP6_MYCTU	O53251	mycobacteri
267	3	50.0	91	1	THIO_THIRO	P96132	thiocapsa r	340	3	50.0	112	1	NIFW_ENTAG	Q52071	enterobacte
268	3	50.0	91	1	YA97_STAAM	Q99v05	staphylococ	341	3	50.0	112	1	VPX_HV2D1	P17760	human immun
269	3	50.0	91	1	YFDM_ECOLI	P76509	escherichia	342	3	50.0	113	1	MEAI_PIG	Q95313	sus scrofa
270	3	50.0	92	1	B2MG_MUSCE	P55078	mus cervico	343	3	50.0	113	1	RBX2_HUMAN	Q9ubf6	homo sapien
271	3	50.0	92	1	B2MG_MUSCR	P55077	mus caroli	344	3	50.0	113	1	RBX2_MOUSE	Q9wtz1	mus musculu
272	3	50.0	92	1	B2MG_MUSSP	Q04714	mus spretus	345	3	50.0	114	1	GTH1_FUNHE	P30971	fundulus he
273	3	50.0	93	1	VAPD_BACNO	Q46565	bacteroides	346	3	50.0	114	1	HV2A_RABIT	P01827	oryctolagus
274	3	50.0	93	1	YQ32_MYCTU	P71931	mycobacteri	347	3	50.0	114	1	YAQD_SCHPO	Q10112	schizosacch
275	3	50.0	94	1	ES66_MYCTU	P95242	mycobacteri	348	3	50.0	114	1	YJ74_AQUAE	O67784	aquifex ao
276	3	50.0	94	1	ESXI_MYCBO	P59802	mycobacteri	349	3	50.0	115	1	CZCI_ALCEU	Q44009	alcaligenes
277	3	50.0	94	1	ESXI_MYCTU	P96364	mycobacteri	350	3	50.0	115	1	MYHA_MOUSE	Q61879	mus musculu
278	3	50.0	94	1	ESXL_MYCBO	P59804	mycobacteri	351	3	50.0	115	1	NPFF_BOVIN	Q9tux7	bos taurus
279	3	50.0	94	1	ESXL_MYCTU	Q05300	mycobacteri	352	3	50.0	115	1	TKN1_RABIT	P41540	oryctolagus
280	3	50.0	94	1	ESXN_MYCTU	O53942	mycobacteri	353	3	50.0	115	1	YAT7_RHOBL	P05450	rhodopsendo
281	3	50.0	95	1	VAPD_ACTAC	Q52243	actinobacil	354	3	50.0	115	1	YEO_ECOLI	P76243	escherichia
282	3	50.0	96	1	NEUY_BRARE	Q9i8p3	brachydanio	355	3	50.0	116	1	HV1A_RABIT	P01826	oryctolagus
283	3	50.0	96	1	YL34_ARCFU	Q28146	archaeoglob	356	3	50.0	116	1	MSCL_STAEP	Q8cpc4	staphylococ
284	3	50.0	97	1	CU83_HSV6U	P52460	human herpe	357	3	50.0	116	1	Y162_ARCFU	O30075	archaeoglob
285	3	50.0	97	1	CU83_HSV6Z	P52461	human herpe	358	3	50.0	116	1	YE94_HABIN	O05071	haemophilus
286	3	50.0	97	1	FIXX_RHISN	Q53207	rhizobium s	359	3	50.0	117	1	ARR1_ECOLI	P15905	escherichia
287	3	50.0	97	1	Y356_METJA	Q57802	methanococc	360	3	50.0	117	1	ARR2_ECOLI	P52144	escherichia
288	3	50.0	97	1	YAN9_YEAST	P39565	saccharomyc	361	3	50.0	117	1	CHBB_CROHO	P81509	crotalus ho
289	3	50.0	98	1	B2MG_MELGA	P21612	meleagris g	362	3	50.0	117	1	HV14_MOUSE	P01758	mus musculu
290	3	50.0	98	1	PHS_RHILO	Q98e92	rhizobium l	363	3	50.0	117	1	HV62_MOUSE	P18533	mus musculu
291	3	50.0	98	1	REGN_BPPH8	P06154	bacterioph	364	3	50.0	117	1	NU3M_LUMTE	Q34950	lumbricus t
292	3	50.0	98	1	VG04_BPMD2	O64200	mycobacteri	365	3	50.0	117	1	NU3M_PROWI	Q37625	prototheca
293	3	50.0	98	1	VG04_BPMLS	Q05251	mycobacteri	366	3	50.0	118	1	ABBB_TRIAB	P81116	trimeresuru
294	3	50.0	98	1	YD22_MYCTU	Q10635	mycobacteri	367	3	50.0	118	1	B2MG_BOVIN	P01888	bos taurus
295	3	50.0	98	1	YDAS_ECOLI	P76063	escherichia	368	3	50.0	118	1	B2MG_HORSE	P30441	equus cabal
296	3	50.0	99	1	B2MG_RABIT	P01885	oryctolagus	369	3	50.0	118	1	B2MG_PIG	Q07717	sus scrofa
297	3	50.0	99	1	GP45_BSPP1	Q48399	bacterioph	370	3	50.0	118	1	HV39_MOUSE	P01809	mus musculu
298	3	50.0	99	1	NOS3_SHEEP	P79209	ovis aries	371	3	50.0	118	1	V118_ASFB7	P18556	african swi
299	3	50.0	99	1	RS6_LACPL	Q890k2	lactobacill	372	3	50.0	118	1	Y380_METJA	Q57825	methanococc
300	3	50.0	99	1	YQJK_ECOLI	Q47710	escherichia	373	3	50.0	118	1	YE16_HABIN	P44188	haemophilus
301	3	50.0	100	1	NOS3_CAVPO	P97270	cavia porce	374	3	50.0	119	1	B2MG_ALOSE	O77523	alouatta se
302	3	50.0	101	1	THI1_CHLTE	Q8kea4	chlorobium	375	3	50.0	119	1	B2MG_AOTAZ	O77537	aotus azara
303	3	50.0	101	1	Y4F3_ENTFA	Q01894	enterococcu	376	3	50.0	119	1	B2MG_AOTNA	O46570	aotus nancy
304	3	50.0	102	1	GTH1_THUOB	P37205	thunnus obe	377	3	50.0	119	1	B2MG_ATEPA	O77536	ateles pani
305	3	50.0	102	1	Y06M_BPT4	P32273	bacterioph	378	3	50.0	119	1	B2MG_BRAAR	O77524	brachyteles
306	3	50.0	102	1	YBEB_HAEIN	P44471	haemophilus	379	3	50.0	119	1	B2MG_CACME	O77533	cacajao mel
307	3	50.0	102	1	YWC8_BACSU	P39600	bacillus su	380	3	50.0	119	1	B2MG_CALEM	O77521	callithrix
308	3	50.0	103	1	C552_NITEU	P95339	nitrosomona	381	3	50.0	119	1	B2MG_CALHO	O77529	callicebus
309	3	50.0	103	1	HEX9_ADECC	Q65944	canine aden	382	3	50.0	119	1	B2MG_CALJA	O77522	callithrix
310	3	50.0	103	1	HEX9_ADECT	P14268	canine aden	383	3	50.0	119	1	B2MG_CALPN	O77528	callicebus
311	3	50.0	103	1	LAC_CHICK	P20763	gallus gall	384	3	50.0	119	1	B2MG_CALPP	O77526	callicebus
312	3	50.0	103	1	MMOD_METCA	P22867	methylococc	385	3	50.0	119	1	B2MG_CALTO	O77530	callicebus
313	3	50.0	103	1	Y944_PYRHO	O58672	pyrococcus	386	3	50.0	119	1	B2MG_CEBAL	O77826	cebus albif
314	3	50.0	104	1	Y019_NPVOP	Q10279	orgyia pseu	387	3	50.0	119	1	B2MG_CEBPY	O77535	cebuella py
315	3	50.0	104	1	YK12_YEAST	P36127	saccharomyc	388	3	50.0	119	1	B2MG_CHISA	O77532	chiropotes
316	3	50.0	105	1	SUGE_CITFR	O69279	citrobacter	389	3	50.0	119	1	B2MG_CRIGR	Q9wv24	cricetulus
317	3	50.0	105	1	THI1_CORNE	P00275	corynebacte	390	3	50.0	119	1	B2MG_HUMAN	P01884	homo sapien
318	3	50.0	105	1	YBEB_ECOLI	P05848	escherichia	391	3	50.0	119	1	B2MG_LAGLA	O77525	lagothrix l
319	3	50.0	106	1	YA43_RHIME	Q92r68	rhizobium m	392	3	50.0	119	1	B2MG_LEOCH	O77519	leontopithe
320	3	50.0	106	1	YDFG_BACNO	P39884	bacteroides	393	3	50.0	119	1	B2MG_MACFA	Q8spw0	macaca fasc
321	3	50.0	107	1	QACH_STASA	O87868	staphylococ	394	3	50.0	119	1	B2MG_MOUSE	P01887	mus musculu
322	3	50.0	107	1	THIO_CHRVI	P09857	chromatium	395	3	50.0	119	1	B2MG_PITIR	O77531	pithecia ir
323	3	50.0	107	1	YF95_HAEIN	P44266	haemophilus	396	3	50.0	119	1	B2MG_PONPY	P16213	pongo pygma
324	3	50.0	108	1	MID1_MUSCR	P82456	mus caroli	397	3	50.0	119	1	B2MG_RAT	P07151	rattus norv
325	3	50.0	108	1	VMEM_LVX	P27331	lily virus	398	3	50.0	119	1	B2MG_SAGBB	O77516	saguinus bi

399	119	1	B2MG_SAGFU	Q9tsx4	saguinus fu	472	3	50.0	132	1	RS11_CHLMU	Q9pjn3	chlamydia m
400	119	1	B2MG_SAGIM	O77518	saguinus im	473	3	50.0	132	1	RS11_CHLTR	P47761	chlamydia t
401	119	1	B2MG_SAGMN	O77517	saguinus mi	474	3	50.0	132	1	RS11_CLOTE	Q890q8	clostridium
402	119	1	B2MG_SAGOE	P55079	saguinus oe	475	3	50.0	132	1	YBL2_STRCI	P33654	streptomyce
403	119	1	B2MG_SAIIB	O77534	saimiri bol	476	3	50.0	132	1	YF83_MYCTU	O06607	mycobacteri
404	119	1	RNP_IGUIG	P80287	iguana igua	477	3	50.0	133	1	CRCB_XYLFT	Q87dk8	xylella fas
405	119	1	YCE2_YEAST	P25572	saccharomyc	478	3	50.0	133	1	FABP_SCHMA	P29498	schistosoma
406	119	1	YG58_METJA	Q59052	methanococc	479	3	50.0	133	1	KV2F_HUMAN	P06310	homo sapien
407	120	1	IAA2_STRGS	P20078	streptomyce	480	3	50.0	133	1	RS11_CHLPN	Q9z7s7	chlamydia p
408	120	1	NU3M_DICDI	Q37312	dictyosteli	481	3	50.0	133	1	RS11_RALSO	Q8xv36	ralstonia s
409	121	1	RA14_CANAL	P53709	candida alb	482	3	50.0	133	1	Y54L_SYNY3	P72777	synechocyst
410	121	1	RBX1_YEAST	Q08273	saccharomyc	483	3	50.0	133	1	YVAD_BACSU	O32226	bacillus su
411	121	1	RS11_UREPA	Q9pqn5	ureaplasma	484	3	50.0	134	1	RS11_COREF	P59371	corynebacte
412	121	1	SRY_RAT	P36394	rattus norv	485	3	50.0	134	1	RS11_CORGL	Q8nsv5	corynebacte
413	121	1	Y198_YERPE	Q8zjb7	yersinia pe	486	3	50.0	134	1	RS11_STRAW	Q82dm3	streptomyce
414	122	1	Y14K_PMV	P20955	papaya mosa	487	3	50.0	134	1	RS11_STRCO	P72403	streptomyce
415	123	1	ABA4_TRIAB	P81114	trimeresuru	488	3	50.0	134	1	VAL3_SLCV	P29049	squash leaf
416	123	1	ECHB_ECHCA	P81996	echis carin	489	3	50.0	135	1	MSRB_AGRF5	Q8ugx7	agrobacteri
417	123	1	IAA2_WHEAT	P01083	triticum ae	490	3	50.0	135	1	RS11_SHEVI	Q9s0r0	shewanella
418	123	1	MECI_STAAN	P26598	staphylococ	491	3	50.0	135	1	VAL2_CLVK	P14976	cassava lat
419	124	1	PRO2_PHYPO	P18322	physarum po	492	3	50.0	135	1	VAL2_CLVN	P14968	cassava lat
420	125	1	ALR_HUMAN	P55789	homo sapien	493	3	50.0	135	1	VAL2_TYLCM	P27263	tomato yell
421	125	1	BOTB_BOTJA	P22030	bothrops ja	494	3	50.0	135	1	VAL2_TYLCU	P38610	tomato yell
422	125	1	SOR_ARCFU	O29903	archaeoglob	495	3	50.0	135	1	VAL2_TYLCV	P27262	tomato yell
423	125	1	VG4_BPPH2	P03682	bacterioph	496	3	50.0	136	1	PSBR_TOBAC	Q40519	nicotiana t
424	125	1	VG4_BPPZA	P06952	bacterioph	497	3	50.0	136	1	RS11_MYCPU	Q98q07	mycoplasma
425	125	1	VG61_BPMD2	O64253	mycobacteri	498	3	50.0	136	1	TVC_HUMAN	Q98q07	mycoplasma
426	125	1	VG61_BPML5	Q05274	mycobacteri	499	3	50.0	136	1	Y07C_BPT4	P03979	homo sapien
427	125	1	Y3C2_STRCO	Q53868	streptomyce	500	3	50.0	136	1	Y16K_CSMV	P13323	bacterioph
428	125	1	YNB3_YEAST	P53979	saccharomyc	501	3	50.0	136	1	Y16K_CSMV	P18919	chloris str
429	126	1	RS11_TREPA	O83241	treponema p	502	3	50.0	137	1	RR11_SPIOL	P17684	caenorhabdi
430	126	1	YTFH_ECOLI	P39316	escherichia	503	3	50.0	137	1	YMAF_BACSU	P06506	spinacia ol
431	127	1	THIO_NEUCR	P42115	neurospora	504	3	50.0	137	1	YMAF_BACSU	Q31794	bacillus su
432	127	1	TRG3_HUMAN	Q9y5p2	homo sapien	505	3	50.0	138	1	ACPS_RALSO	Q8y0h7	ralstonia s
433	127	1	YCT3_YEAST	P25361	saccharomyc	505	3	50.0	138	1	CH16_DROME	P22977	drosophila
434	128	1	YMJ0_YEAST	Q04501	saccharomyc	506	3	50.0	138	1	CSGF_ECOLI	P52104	escherichia
435	129	1	IR08_HCMVA	P16806	human cytom	507	3	50.0	138	1	R14A_YEAST	P36105	saccharomyc
436	129	1	NUSB_STAEP	O8cp37	staphylococ	508	3	50.0	138	1	R14B_YEAST	P38754	saccharomyc
437	129	1	RS11_BACHD	O50633	bacillus ha	509	3	50.0	138	1	RR9_ODOSI	P49497	odontella s
438	129	1	RS11_NITEU	Q82x71	nitrosomona	510	3	50.0	138	1	VGAM_LAMBD	P03702	bacterioph
439	129	1	RS11_PSEAE	Q9hvf8	pseudomonas	511	3	50.0	139	1	CH16_DROVI	P24512	drosophila
440	129	1	RS11_PSEPK	P59374	pseudomonas	512	3	50.0	139	1	RBS_FLECA	Q08052	pleurochrys
441	129	1	RS11_PSESM	Q889u8	pseudomonas	513	3	50.0	139	1	Y965_MYCTU	P71545	mycobacteri
442	129	1	VAF2_DROME	Q9vnl3	drosophila	514	3	50.0	140	1	CO8B_RAT	P55314	rattus norv
443	130	1	DHSC_PARDE	Q59659	paracoccus	515	3	50.0	140	1	REL3_RAT	Q8bfs3	rattus norv
444	130	1	GLOV_HYACE	P81048	hyalophora	516	3	50.0	140	1	YQIB_ECOLI	P36652	escherichia
445	130	1	LVIG_HUMAN	P06316	homo sapien	517	3	50.0	141	1	CH16_DROSU	P24511	drosophila
446	130	1	MIA_MOUSE	Q61865	mus musculu	518	3	50.0	141	1	FABP_ANOGA	Q17017	anopheles g
447	130	1	NLR_DESGI	O50258	desulfovibr	519	3	50.0	142	1	REL3_MOUSE	Q8chk2	mus musculu
448	130	1	RR11_ODOSI	P49499	odontella s	520	3	50.0	142	1	GLB1_LUCPE	P41260	lucina pect
449	130	1	RS11_SHEON	P59375	shewanella	521	3	50.0	142	1	NUSB_STRCO	Q9kxr0	streptomyce
450	130	1	RS11_SYNP6	O24709	synechococc	522	3	50.0	142	1	NXT2_HUMAN	Q9npj8	homo sapien
451	130	1	RS11_SYNP3	P73298	synechocyst	523	3	50.0	142	1	OC17_CHICK	Q9prs8	gallus gall
452	130	1	RS11_XANCP	Q9z3e9	xanthomonas	524	3	50.0	142	1	PTP_AC1JO	O52787	acinetobact
453	130	1	TKN1_BOVIN	P01289	bos taurus	525	3	50.0	142	1	RPB6_SCHPO	P36595	schizosacch
454	130	1	TKN1_MESAU	Q60541	mesocricetu	526	3	50.0	142	1	U426_HSVMG	Q05104	marek's dis
455	130	1	TKN1_MOUSE	P41539	mus musculu	527	3	50.0	143	1	CRCB_XYLFA	Q9pdcs	xylella fas
456	130	1	TKN1_MOUSE	P06767	rattus norv	528	3	50.0	143	1	IL3_MACMU	P25140	macaca mula
457	130	1	UCR6_ECHMU	Q9gp40	echinococcu	529	3	50.0	144	1	FLAV_TRIER	O52659	trichodesmi
458	130	1	YQ56_MYCTU	P71953	mycobacteri	530	3	50.0	144	1	GLB_APLJU	P14393	aplysia jul
459	131	1	ABA1_TRIAB	P81111	trimeresuru	531	3	50.0	144	1	GLB_APLKU	P02211	aplysia kur
460	131	1	ATPN_CAEEL	Q18803	caenorhabdi	532	3	50.0	144	1	NUSB_HAEIN	P45150	haemophilus
461	131	1	ATPO_CAEEL	P90921	caenorhabdi	533	3	50.0	144	1	NUSB_STRAW	Q827r4	streptomyce
462	131	1	FRDC_PROVU	P20923	proteus vul	534	3	50.0	144	1	RL15_SULAC	O05643	sulfolobus
463	131	1	OREX_HUMAN	Q43612	homo sapien	535	3	50.0	144	1	RL15_SULSO	Q9ux85	sulfolobus
464	131	1	OREX_PIG	O77668	sus scrofa	536	3	50.0	144	1	VMTT_LAMBD	P03735	bacterioph
465	131	1	RPB6_DROME	Q24320	drosophila	537	3	50.0	144	1	YCD3_METFE	Q93733	methanother
466	131	1	RS11_ANASP	Q8ypk2	anabaena sp	538	3	50.0	145	1	ENPP_BPP22	P13583	bacterioph
467	131	1	RS11_NEIMA	Q9jqr2	neisseria m	539	3	50.0	145	1	GT22_DIACA	Q03425	dianthus ca
468	132	1	ABBA_TRIAB	P81115	trimeresuru	540	3	50.0	145	1	IAAA_HORVU	P28041	hordeum vul
469	132	1	HEX9_ADE40	P48312	human adeno	541	3	50.0	145	1	LYC_OPHO	Q91159	opisthocomu
470	132	1	MRKF_KLEPN	P21650	klebsiella	542	3	50.0	145	1	NUIM_TRYBB	P30826	trypanosoma
471	132	1	RS11_CHLCV	Q824n2	chlamydophi	543	3	50.0	145	1	SYCN_MOUSE	Q8vck7	mus musculu
						544	3	50.0	145	1	SYCN_RAT	O35775	rattus norv

Q9pjn3	chlamydia m
P47761	chlamydia t
Q890q8	clostridium
P33654	streptomyce
O06607	mycobacteri
Q87dk8	xylella fas
P29498	schistosoma
P06310	homo sapien
Q9z7s7	chlamydia p
Q8xv36	ralstonia s
P72777	synechocyst
O32226	bacillus su
P59371	corynebacte
Q8nsv5	corynebacte
Q82dm3	streptomyce
P72403	streptomyce
P29049	squash leaf
Q8ugx7	agrobacteri
Q9s0r0	shewanella
P14976	cassava lat
P14968	cassava lat
P27263	tomato yell
P38610	tomato yell
P27262	tomato yell
Q40519	nicotiana t
Q98q07	mycoplasma
P03979	homo sapien
P13323	bacterioph
P18919	chloris str
P17684	caenorhabdi
P06506	spinacia ol
Q31794	bacillus su
Q8y0h7	ralstonia s
P22977	drosophila
P52104	escherichia
P36105	saccharomyc
P38754	saccharomyc
P49497	odontella s
P03702	bacterioph
P24512	drosophila
Q08052	pleurochrys
P71545	mycobacteri
P55314	rattus norv
Q8bfs3	rattus norv
P36652	escherichia
P24511	drosophila
Q17017	anopheles g
Q8chk2	mus musculu
P41260	lucina pect
Q9kxr0	streptomyce
Q9npj8	homo sapien
Q9prs8	gallus gall
O52787	acinetobact
P36595	schizosacch
Q05104	marek's dis
Q9pdcs	xylella fas
P25140	macaca mula
O52659	trichodesmi
P14393	aplysia jul
P02211	aplysia kur
P45150	haemophilus
Q827r4	streptomyce
O05643	sulfolobus
Q9ux85	sulfolobus
P03735	bacterioph
Q93733	methanother
P13583	bacterioph
Q03425	dianthus ca
P28041	hordeum vul
Q91159	opisthocomu
P30826	trypanosoma
Q8vck7	mus musculu
O35775	rattus norv

545	3	50.0	145	1	VPRE_HUMAN	P12018 homo sapien
546	3	50.0	145	1	YAC1_METSO	P27096 methanothri
547	3	50.0	145	1	YCEA_PAEAL	P29718 paenibacill
548	3	50.0	146	1	CYM5_RAT	P04166 rattus norv
549	3	50.0	146	1	GLB_APLLI	P02210 aplysia lim
550	3	50.0	146	1	GLB_BURLE	P29287 bursatella
551	3	50.0	146	1	HV2I_HUMAN	P06331 homo sapien
552	3	50.0	146	1	IXB_TRIFL	P23807 trimeresuru
553	3	50.0	146	1	MMHB_AKGHA	Q9yi92 agkistrodon
554	3	50.0	146	1	MOAB_RHOSH	Q53091 rhodobacter
555	3	50.0	147	1	CST9_HUMAN	Q9h4g1 homo sapien
556	3	50.0	147	1	GS17_XENLA	P07733 xenopus lae
557	3	50.0	147	1	Y565_METJA	Q57985 methanococc
558	3	50.0	148	1	GLB3_TYLHE	P13578 tyloxyrhynch
559	3	50.0	148	1	HUPG_BRAJA	P48339 bradyrhizob
560	3	50.0	148	1	LYC1_RAT	P00697 rattus norv
561	3	50.0	148	1	LYCM_MOUSE	P08905 mus musculu
562	3	50.0	148	1	LYCP_MOUSE	P17897 mus musculu
563	3	50.0	148	1	MYG_GALGA	P14397 galeorhinus
564	3	50.0	148	1	REGQ_BPAPS	Q9tlu3 bacterioph
565	3	50.0	148	1	RS19_EMENI	P27073 emericeella
566	3	50.0	148	1	SSRP_NEIMA	Q51111 neisseria m
567	3	50.0	148	1	UBCC_SCHPO	O13685 schizosacch
568	3	50.0	148	1	Y18K_MSVS	P14989 maize strea
569	3	50.0	148	1	YF58_MYCTU	Q10772 mycobacteri
570	3	50.0	148	1	YK83_YERPE	Q8zes0 yersinia pe
571	3	50.0	148	1	YORX_PYRWO	P20298 pyrococcus
572	3	50.0	149	1	HUPG_RHILV	P28149 rhizobium l
573	3	50.0	149	1	NDK1_SACOF	P93554 saccharum o
574	3	50.0	149	1	YGAW_ECOLI	P76626 escherichia
575	3	50.0	150	1	NUFM_CAEEL	Q18359 caenorhabdi
576	3	50.0	150	1	R19E_THEAC	Q9hm21 thermoplas
577	3	50.0	150	1	TCPQ_VIBCH	P29490 vibrio chol
578	3	50.0	150	1	VHR2_CAMPS	Q8v228 camelpox vi
579	3	50.0	150	1	VHR2_MONPV	Q8v566 monkeypox v
580	3	50.0	150	1	VHR2_VACCV	P17363 vaccinia vi
581	3	50.0	150	1	VHR2_VARV	P33860 variola vir
582	3	50.0	151	1	CT78_HUMAN	Q9br46 homo sapien
583	3	50.0	151	1	LE14_GOSHI	P46518 gossypium h
584	3	50.0	151	1	Y4JR_RHISN	P55518 rhizobium s
585	3	50.0	152	1	CYPC_STRCN	Q02572 streptomyce
586	3	50.0	152	1	LE14_SOYBN	P46519 glycine max
587	3	50.0	152	1	LUXS_HELPJ	Q9zmw8 helicobacte
588	3	50.0	152	1	RS15_ARCFJ	Q29457 archaeoglob
589	3	50.0	152	1	TPC_PATYE	P35622 patinopecte
590	3	50.0	153	1	ENPP_BPP21	P27358 bacterioph
591	3	50.0	153	1	ENPP_LAMBD	P00726 bacterioph
592	3	50.0	153	1	RECX_PSEAE	P37860 pseudomonas
593	3	50.0	153	1	RS15_METJA	P54012 methanococc
594	3	50.0	153	1	RZPD_ECOLI	P75719 escherichia
595	3	50.0	153	1	Y18K_MSVN	P14978 maize strea
596	3	50.0	153	1	YCGN_SALTI	Q8z682 salmonella
597	3	50.0	153	1	YCGN_SALTY	Q8z612 salmonella
598	3	50.0	154	1	AR16_YEAST	P40518 saccharomyc
599	3	50.0	154	1	CORZ_DROME	Q26377 drosophila
600	3	50.0	154	1	MER2_EUPOC	O15825 euplotes oc
601	3	50.0	154	1	Y451_SYNY3	P74676 synechocyst
602	3	50.0	154	1	YHAV_ECOLI	P42901 escherichia
603	3	50.0	155	1	LUXS_HELPY	O24931 helicobacte
604	3	50.0	155	1	MOAC_COREF	Q8fu35 corynebacte
605	3	50.0	155	1	RPB6_YEAST	P20435 saccharomyc
606	3	50.0	155	1	YC36_GUITH	O78501 guillardia
607	3	50.0	156	1	CDN2_HUMAN	P42771 homo sapien
608	3	50.0	156	1	MOAC_CORGL	Q8ntu1 corynebacte
609	3	50.0	156	1	NUKM_PARTE	P15602 paramecium
610	3	50.0	156	1	PM20_SCHPO	O14313 schizosacch
611	3	50.0	156	1	SOXR_PSEAE	Q51506 pseudomonas
612	3	50.0	156	1	VPG_PLRV	P10471 potato leaf
613	3	50.0	156	1	VPG_PLRV1	P17524 potato leaf
614	3	50.0	156	1	VPG_PLRVR	P17523 potato leaf
615	3	50.0	156	1	VPG_PLRVW	P11625 potato leaf
616	3	50.0	156	1	YQ69_MYCTU	P71966 mycobacteri
617	3	50.0	157	1	GLB1_PARCH	P15161 paracaudina

618	3	50.0	157	1	MMHA_AKGHA	Q9ygg9 agkistrodon
619	3	50.0	157	1	NDK_PYRHO	O58429 pyrococcus
620	3	50.0	157	1	SSRP_BRAJA	Q9rh74 bradyrhizob
621	3	50.0	157	1	UL51_HCMVA	P16792 human cytom
622	3	50.0	157	1	YIAM_ECOLI	P37674 escherichia
623	3	50.0	157	1	YWMA_BACSU	P70958 bacillus su
624	3	50.0	158	1	CU14_HUMAN	P56557 homo sapien
625	3	50.0	158	1	CU14_MOUSE	Q9dlx9 mus musculu
626	3	50.0	158	1	GLB1_CHITH	P02221 chironomus
627	3	50.0	158	1	RNKD_SGOE	P47786 saguinus oe
628	3	50.0	159	1	CYPC_STRCO	P23154 streptomyce
629	3	50.0	159	1	SSRP_RHILV	Q985b9 rhizobium l
630	3	50.0	159	1	YHA6_YEAST	P38751 saccharomyc
631	3	50.0	160	1	GLB2_CHITH	P02222 chironomus
632	3	50.0	160	1	GREB_VIBVU	Q8ddu7 vibrio vuln
633	3	50.0	160	1	RRAL_VIBPA	Q87ed2 vibrio para
634	3	50.0	160	1	RRAL_VIBVU	Q8dep0 vibrio vuln
635	3	50.0	160	1	RT2C_ACTPL	P15376 actinobacil
636	3	50.0	160	1	Y4FE_RHISN	P55443 rhizobium s
637	3	50.0	160	1	YCDZ_SALTY	O54290 salmonella
638	3	50.0	160	1	YFIB_ECOLI	P07021 escherichia
639	3	50.0	161	1	GLB9_CHITH	P02223 chironomus
640	3	50.0	161	1	GREB_VIBCH	Q9kn17 vibrio chol
641	3	50.0	161	1	HLB_TRETO	P07803 trema tomen
642	3	50.0	161	1	NDK_PYRFU	Q8u2a8 pyrococcus
643	3	50.0	161	1	RRAL_VIBCH	Q9kpk1 vibrio chol
644	3	50.0	162	1	CVPA_ECOLI	P08550 escherichia
645	3	50.0	162	1	HLB_HORVU	Q42831 hordeum vul
646	3	50.0	162	1	IPYR_MYCLE	O69540 mycobacteri
647	3	50.0	162	1	IPYR_MYCTU	O06379 mycobacteri
648	3	50.0	162	1	RECX_XANOR	Q8ap31 xanthomonas
649	3	50.0	162	1	YPU1_RHOCA	P26157 rhodobacter
650	3	50.0	163	1	GLBZ_CHITH	P23761 chironomus
651	3	50.0	163	1	IPYR_STRCO	P29245 chironomus
652	3	50.0	163	1	PUR6_PSEAE	Q9x819 streptomyce
653	3	50.0	163	1	YCDZ_ECOLI	P72157 pseudomonas
654	3	50.0	164	1	PR12_HORVU	P75916 escherichia
655	3	50.0	164	1	PR13_HORVU	P35792 hordeum vul
656	3	50.0	164	1	PR1_HORVU	P35793 hordeum vul
657	3	50.0	164	1	YOJ3_CAEEL	Q05968 hordeum vul
658	3	50.0	164	1	CTE1_HUMAN	P34626 caenorhabdi
659	3	50.0	165	1	HLB_MAIZE	Q9nub4 homo sapien
660	3	50.0	165	1	HLB_ZEAMP	Q9fy42 zea mays (s
661	3	50.0	165	1	LITI_MOUSE	Q9m593 zea mays (s
662	3	50.0	165	1	LITH_RAT	P43137 mus musculu
663	3	50.0	165	1	LKTC_PASSP	P10758 rattus norv
664	3	50.0	165	1	YRH1_RHOSH	P55124 pasteurella
665	3	50.0	165	1	HLB1_ORYSA	Q53229 rhodobacter
666	3	50.0	166	1	PAL_PSEPK	O04986 oryza sativ
667	3	50.0	166	1	RECX_SALTY	P43036 pseudomonas
668	3	50.0	166	1	RECX_SALTI	Q8z4d4 salmonella
669	3	50.0	166	1	HLB4_ORYSA	Q8zmk5 salmonella
670	3	50.0	167	1	LKC1_PASHA	Q94ft7 oryza sativ
671	3	50.0	167	1	LKC3_PASHA	P16533 pasteurella
672	3	50.0	167	1	LKCB_PASHA	P55120 pasteurella
673	3	50.0	167	1	VHR2_YABAM	P55121 pasteurella
674	3	50.0	167	1	LKTC_ACTAC	Q9qbb4 yaba monkey
675	3	50.0	168	1	PSA_DICDI	P16461 actinobacil
676	3	50.0	168	1	VVHB_VIBVU	P12729 dictyosteli
677	3	50.0	168	1	YCIE_ECOLI	P19248 vibrio vuln
678	3	50.0	168	1	YY22_MYCTU	P21363 escherichia
679	3	50.0	168	1	CX41_THUOB	Q50706 mycobacteri
680	3	50.0	169	1	HLB2_ORYSA	Q918u0 thunnus obe
681	3	50.0	169	1	HLB3_ORYSA	O04985 oryza sativ
682	3	50.0	169	1	LFS_ALLCE	Q94ft8 oryza sativ
683	3	50.0	169	1	NAPB_ALCEU	P59082 allium cepa
684	3	50.0	169	1	RIMM_NEIMA	P39186 alcaligenes
685	3	50.0	169	1	RIMM_NEIMB	Q9jvk9 neisseria m
686	3	50.0	169	1	YIST_BACSU	Q9k0k3 neisseria m
687	3	50.0	169	1	HLC1_ECOLI	O07939 bacillus su
688	3	50.0	170	1	HLVC_ECOLI	P09984 escherichia
689	3	50.0	170	1	VEAR_HCMVA	P06736 escherichia
690	3	50.0	170	1		P09694 human cytom

691	3	50.0	171	1	HUNB_SCAAL	O46254	scaptomyza
692	3	50.0	171	1	PUR6_MYCLE	P46702	mycobacteri
693	3	50.0	172	1	CX42_RAT	Q91y94	rattus norv
694	3	50.0	172	1	MEA1_HUMAN	Q16626	homo sapien
695	3	50.0	172	1	RT1C_ACTPL	P55i32	actinobacil
696	3	50.0	172	1	UL45_HSV11	P10229	herpes simp
697	3	50.0	172	1	UL45_HSV1K	P28987	herpes simp
698	3	50.0	172	1	UL45_HSV1M	P06482	herpes simp
699	3	50.0	172	1	Y856_PYRHO	Q58586	pyrococcus
700	3	50.0	172	1	YC46_PYRAB	Q9uza8	pyrococcus
701	3	50.0	173	1	CLF8_HUMAN	Q8izv2	homo sapien
702	3	50.0	173	1	CLF8_MOUSE	Q9c2r4	mus musculus
703	3	50.0	173	1	FLAV_HAEIN	P44562	haemophilus
704	3	50.0	173	1	LIT2_MOUSE	Q08731	mus musculus
705	3	50.0	173	1	NU6M_SCYCA	O79412	scyliorhinu
706	3	50.0	173	1	NU6M_SQUAC	Q9zz43	squalus aca
707	3	50.0	173	1	NUDH_RHILO	Q98f04	rhizobium l
708	3	50.0	173	1	RT3C_ACTPL	Q04474	actinobacil
709	3	50.0	173	1	YO13_BPHP1	P51715	bacterioph
710	3	50.0	174	1	HLC2_ECOLI	P09985	escherichia
711	3	50.0	174	1	MEA1_BOVIN	Q29407	bos taurus
712	3	50.0	174	1	MEAL_MOUSE	Q64327	mus musculus
713	3	50.0	174	1	NUOB_RICPR	Q9zd82	rickettsia
714	3	50.0	174	1	PADC_VIBCH	Q9kpx2	vibrio chol
715	3	50.0	174	1	PYRR_RALSO	O8y1l3	ralstonia s
716	3	50.0	175	1	CT38_HUMAN	Q9nuv7	homo sapien
717	3	50.0	175	1	DIAC_BOVIN	Q01458	bos taurus
718	3	50.0	175	1	FLAV_SHIFL	Q83880	shigella fl
719	3	50.0	175	1	NUGC_ANASP	Q44241	anabaena sp
720	3	50.0	175	1	NUGC_ANAVA	Q9xb16	anabaena va
721	3	50.0	176	1	C552_PARDE	P54820	paracoccus
722	3	50.0	176	1	VA22_VACCC	P20997	vaccinia vi
723	3	50.0	177	1	CRAB_SQUAC	P02512	squalus aca
724	3	50.0	177	1	OM19_BRUME	Q44663	brucella me
725	3	50.0	177	1	Y086_METMA	Q8q0q0	methanosarc
726	3	50.0	177	1	YH86_ARCFU	O28488	archaeoglob
727	3	50.0	178	1	DSBB_VIBPA	Q87n03	vibrio para
728	3	50.0	178	1	VHR2_YLDV	Q9dhp6	yaba-like d
729	3	50.0	179	1	CAS2_RAT	P02667	rattus norv
730	3	50.0	179	1	NUGC_SINY3	P19125	synecocyst
731	3	50.0	179	1	PYRE_MYCTU	O53717	mycobacteri
732	3	50.0	179	1	YGJP_ECOLI	P42597	escherichia
733	3	50.0	180	1	CYSH_RHITR	Q33579	rhizobium t
734	3	50.0	180	1	ISPZ_YERPE	Q8zeh5	yersinia pe
735	3	50.0	180	1	TXLA_SINY3	P73920	synecocyst
736	3	50.0	180	1	Y554_HAEIN	P44014	haemophilus
737	3	50.0	180	1	YC55_PYRHO	O58998	pyrococcus
738	3	50.0	180	1	YW60_XANCP	Q8p586	xanthomonas
739	3	50.0	180	1	YY06_XANAC	Q8pb54	xanthomonas
740	3	50.0	181	1	AAC2_MYCTU	P95219	mycobacteri
741	3	50.0	181	1	CHMU_ERWHE	P42517	erwinia her
742	3	50.0	181	1	FANC_ECOLI	P18103	escherichia
743	3	50.0	181	1	TRBB_ECOLI	P18035	escherichia
744	3	50.0	181	1	Y06E_BPT4	P13311	bacterioph
745	3	50.0	181	1	VV17_METAC	Q8t1c0	methanosarc
746	3	50.0	182	1	YNJA_ECOLI	P52627	escherichia
747	3	50.0	183	1	FLIZ_ECOLI	Q98qp6	mycoplasma
748	3	50.0	183	1	IPYR_MYCPU	Q05286	mycobacteri
749	3	50.0	183	1	VG71_BPML5	Q8nm11	corynebacte
750	3	50.0	184	1	PYRE_CORGL	P46452	haemophilus
751	3	50.0	184	1	YAED_HAEIN	Q9vh95	drosophila
752	3	50.0	184	1	YC17_DROME	Q45359	bordetella
753	3	50.0	185	1	CYAC_BORPE	P39250	bacterioph
754	3	50.0	185	1	END4_BPT4	Q37875	bacterioph
755	3	50.0	185	1	LYCV_BPP1	Q56460	paracoccus
756	3	50.0	186	1	MAUE_PARVE	P14123	haloarcula
757	3	50.0	186	1	RL18_HALMA	P33494	turkey rhin
758	3	50.0	186	1	VMA2_TRTV	Q10869	mycobacteri
759	3	50.0	186	1	YJ89_MYCTU	P33490	nicotiana t
760	3	50.0	187	1	ABP1_TOBAC	P33491	nicotiana t
761	3	50.0	187	1	ABP2_TOBAC	P82973	enterobacte
762	3	50.0	187	1	AMPD_ENTCL	O00746	homo sapien
763	3	50.0	187	1	NDKM_HUMAN		

764	3	50.0	187	1	NIP3_MOUSE	O55003	mus musculu
765	3	50.0	187	1	VA22_VARV	P33845	variola vir
766	3	50.0	187	1	YK06_AERPE	Q9yad3	aeropyrum p
767	3	50.0	188	1	INL6_RAT	Q9wv41	rattus norv
768	3	50.0	188	1	RL5_PYRAB	Q9viu9	pyrococcus
769	3	50.0	188	1	RL5_PYRHO	O59431	pyrococcus
770	3	50.0	188	1	SPR_ECOLI	P77685	escherichia
771	3	50.0	188	1	UBCB_YEAST	P52491	saccharomyc
772	3	50.0	189	1	BBP_FIEBR	P09464	piensis bras
773	3	50.0	189	1	NCSI_YEAST	Q06389	saccharomyc
774	3	50.0	189	1	Y064_METJA	Q60376	methanococc
775	3	50.0	189	1	YMFL_ECOLI	P75976	escherichia
776	3	50.0	189	1	YWOC_BACSU	P94573	bacillus su
777	3	50.0	190	1	PHB2_HUMAN	Q9ue74	homo sapien
778	3	50.0	190	1	VE03_VACCC	P21081	vaccinia vi
779	3	50.0	190	1	VE03_VACCV	P21605	vaccinia vi
780	3	50.0	190	1	VE03_VARV	P33863	variola vir
781	3	50.0	191	1	INL6_MOUSE	Q9gy05	mus musculu
782	3	50.0	191	1	RT11_MOUSE	Q9dca2	mus musculu
783	3	50.0	191	1	THIF_MESCR	O81332	mesembryant
784	3	50.0	191	1	TXLA_SINP7	P35088	synechococc
785	3	50.0	191	1	YAED_ECOLI	P31546	escherichia
786	3	50.0	192	1	KITH_VIBCH	Q9k8t9	vibrio chol
787	3	50.0	192	1	KITH_VIBPA	Q87qj8	vibrio para
788	3	50.0	192	1	KITH_VIBVU	Q8d8r2	vibrio vuln
789	3	50.0	192	1	MOBA_NEIMA	Q9juas	neisseria m
790	3	50.0	192	1	MOBA_NEIMB	P58747	neisseria m
791	3	50.0	192	1	RR4B_CVACA	O22029	cyanidium c
792	3	50.0	193	1	BCLW_HUMAN	Q92843	homo sapien
793	3	50.0	193	1	BCLW_MOUSE	P70345	mus musculu
794	3	50.0	193	1	DEF2_COREF	O8fmd0	corynebacte
795	3	50.0	193	1	TSAL_MOUSE	Q9d9t6	mus musculu
796	3	50.0	193	1	YBF9_YEAST	P34224	saccharomyc
797	3	50.0	194	1	COX2_PARDE	P08303	paracoccus
798	3	50.0	194	1	MOBA_SINP7	O06866	synechococc
799	3	50.0	194	1	NIP3_HUMAN	Q12983	homo sapien
800	3	50.0	195	1	AAC2_MYCFO	Q49157	mycobacteri
801	3	50.0	195	1	FOS_SHEEP	O02761	ovis aries
802	3	50.0	195	1	YFIK_ECOLI	P38101	escherichia
803	3	50.0	196	1	NODA_MESPL	O8vvh1	mesorhizobi
804	3	50.0	196	1	NODA_MESS7	Q9ran9	mesorhizobi
805	3	50.0	196	1	NODA_RHIGA	P50348	rhizobium g
806	3	50.0	196	1	NODA_RHILT	P04673	rhizobium l
807	3	50.0	196	1	NODA_RHIME	P02962	rhizobium m
808	3	50.0	196	1	NODA_RHISN	P50349	rhizobium s
809	3	50.0	196	1	NODA_RHITR	Q53252	rhizobium t
810	3	50.0	196	1	NODA_SINTE	Q8vvf0	sinorhizobi
811	3	50.0	196	1	RS7_AERPE	Q9yau8	aeropyrum p
812	3	50.0	196	1	YJAG_HABIN	P44709	haemophilus
813	3	50.0	196	1	YM87_CORGL	Q8nnb7	corynebacte
814	3	50.0	197	1	COAE_BACSU	O34932	bacillus su
815	3	50.0	197	1	COP9_ARATH	P43255	arabidopsis
816	3	50.0	197	1	NODA_RHILO	Q52839	rhizobium l
817	3	50.0	197	1	NUOC_NEIMA	Q9jx80	neisseria m
818	3	50.0	197	1	NUOC_NEIMB	Q9k1c1	neisseria m
819	3	50.0	197	1	TMRB_BACSU	P12921	bacillus su
820	3	50.0	197	1	UL52_HSVE4	Q00040	equine herp
821	3	50.0	197	1	YK45_YEAST	P36147	saccharomyc
822	3	50.0	197	1	YRPA_SINPZ	Q02426	synechococc
823	3	50.0	198	1	COX2_NOTPE	O03892	nothoprocta
824	3	50.0	198	1	COX2_TINMA	O03895	tinamus maj
825	3	50.0	198	1	OPNR_AGRHH	P27872	agrobacteri
826	3	50.0	198	1	PGD2_CHICK	O73888	gallus gall
827	3	50.0	198	1	PGD2_HUMAN	O60760	homo sapien
828	3	50.0	198	1	PGD2_MOUSE	Q9jhf7	mus musculu
829	3	50.0	198	1	PGD2_RAT	Q35543	rattus norv
830	3	50.0	198	1	VH23_SFVKA	Q9q907	shope fibro
831	3	50.0	198	1	YJV7_YEAST	P40893	saccharomyc
832	3	50.0	198	1	YR71_ECOLI	P21323	escherichia
833	3	50.0	199	1	CD69_MOUSE	P37217	mus musculu
834	3	50.0	199	1	COX2_APTAU	O03889	apteryx aus
835	3	50.0	199	1	COX2_CASBE	O03890	casuarius b
836	3	50.0	199	1	COX2_DRONO	O03891	dromaius no

Q46254	scaptomyza
P46702	mycobacteri
Q91y94	rattus norv
Q16626	homo sapien
P55i32	actinobacil
P10229	herpes simp
P28987	herpes simp
P06482	herpes simp
Q58586	pyrococcus
Q9uza8	pyrococcus
Q8izv2	homo sapien
Q9c2r4	mus musculus
P44562	haemophilus
Q08731	mus musculus
O79412	scyliorhinu
Q9zz43	squalus aca
Q98f04	rhizobium l
Q04474	actinobacil
P51715	bacterioph
P09985	escherichia
Q29407	bos taurus
Q64327	mus musculus
Q9zd82	rickettsia
Q9kpx2	vibrio chol
O8y1l3	ralstonia s
Q9nuv7	homo sapien
Q01458	bos taurus
Q83880	shigella fl
Q44241	anabaena sp
Q9xb16	anabaena va
P54820	paracoccus
P20997	vaccinia vi
P02512	squalus aca
Q44663	brucella me
Q8q0q0	methanosarc
O28488	archaeoglob
Q87n03	vibrio para
Q9dhp6	yaba-like d
P02667	rattus norv
P19125	synecocyst
O53717	mycobacteri
P42597	escherichia
Q33579	rhizobium t
Q8zeh5	yersinia pe
P73920	synecocyst
P44014	haemophilus
O58998	pyrococcus
Q8p586	xanthomonas
Q8pb54	xanthomonas
P95219	mycobacteri
P42517	erwinia her
P18103	escherichia
P18035	escherichia
P13311	bacterioph
Q8t1c0	methanosarc
P52627	escherichia
Q98qp6	mycoplasma
Q05286	mycobacteri
Q8nm11	corynebacte
P46452	haemophilus
Q9vh95	drosophila
Q45359	bordetella
P39250	bacterioph
Q37875	bacterioph
Q56460	paracoccus
P14123	haloarcula
P33494	turkey rhin
Q10869	mycobacteri
P33490	nicotiana t
P33491	nicotiana t
P82973	enterobacte
O00746	homo sapien

837	3	50.0	199	1	COX2_RHEAM	O03893	rhea americ	910	3	50.0	211	1	NDK5_MOUSE	Q99mh5	mus musculu
838	3	50.0	199	1	NHAA_PSECL	P27764	pseudomonas	911	3	50.0	211	1	THIE_ECO57	Q8x6y0	escherichia
839	3	50.0	199	1	RS4_MYCPU	Q98pk6	mycoplasma	912	3	50.0	211	1	THIE_ECOL6	Q8fb78	escherichia
840	3	50.0	199	1	RS8_YEAST	P05754	saccharomyc	913	3	50.0	211	1	THIE_ECOLI	P30137	escherichia
841	3	50.0	199	1	Y266_HAEIN	P44603	haemophilus	914	3	50.0	211	1	THIE_SALTI	Q8z325	salmonella
842	3	50.0	199	1	Y269_SYNY3	P73888	synechocyst	915	3	50.0	211	1	THIE_SALTY	Q91918	salmonella
843	3	50.0	199	1	YE74_HAEIN	Q57213	haemophilus	916	3	50.0	211	1	TRPF_PSEAE	Q59649	pseudomonas
844	3	50.0	200	1	NUPL_XENLA	P05221	xenopus lae	917	3	50.0	211	1	TX10_HUMAN	O75333	homo sapien
845	3	50.0	200	1	VATE_BORBU	O51123	borrelia bu	918	3	50.0	211	1	YNQ8_CAEEL	Q21984	caenorhabdi
846	3	50.0	200	1	YL86_COREF	Q8fnf8	corynebacte	919	3	50.0	211	1	ZFP5_ARATH	Q39264	arabidopsis
847	3	50.0	201	1	ABP1_MAIZE	P13689	zea mays (m	920	3	50.0	212	1	GRPE_LEPIN	O51868	leptospira
848	3	50.0	201	1	HAM1_LACLA	Q9cg29	lactococcus	921	3	50.0	212	1	KTHY_SYNY3	Q55593	synechocyst
849	3	50.0	201	1	NUC1_RHIME	O68854	rhizobium m	922	3	50.0	212	1	NDK5_HUMAN	P56597	homo sapien
850	3	50.0	201	1	OM25_BRUOV	Q45335	brucella ov	923	3	50.0	212	1	PPIC_HUMAN	P45877	homo sapien
851	3	50.0	201	1	ULC0_HCMVA	P16740	human cytom	924	3	50.0	212	1	PYEL_HALN1	Q9ha16	halobacteri
852	3	50.0	201	1	YPA2_LEGPN	P26881	legionella	925	3	50.0	212	1	TAL_BACSU	P19669	bacillus su
853	3	50.0	202	1	COAE_CHLMU	Q9pjp9	chlamydia m	926	3	50.0	212	1	USO1_HCMVA	P09714	human cytom
854	3	50.0	202	1	COAE_CHLTR	O84499	chlamydia t	927	3	50.0	213	1	CPCF_SYNEL	P50038	synechococc
855	3	50.0	202	1	LEXA_ERWCA	Q04596	erwinia car	928	3	50.0	213	1	HIS1_BACSU	O34520	bacillus su
856	3	50.0	202	1	NQRE_PSEAE	Q9hz10	pseudomonas	929	3	50.0	213	1	OM25_BRUAB	Q44664	brucella ab
857	3	50.0	202	1	RNFG_PASMU	Q9cnp4	pasteurella	930	3	50.0	213	1	OM25_BRUCA	Q45110	brucella ca
858	3	50.0	202	1	YJ72_YEAST	P47142	saccharomyc	931	3	50.0	213	1	OM25_BRUME	Q45321	brucella me
859	3	50.0	203	1	CLDM_HUMAN	Q8n7p3	homo sapien	932	3	50.0	213	1	OM25_BRUNE	Q45326	brucella ne
860	3	50.0	203	1	FMS5_ECOLI	P33781	escherichia	933	3	50.0	213	1	OM25_BRUSU	Q45689	brucella su
861	3	50.0	203	1	GTS_OMSL	P46088	ommastrephe	934	3	50.0	213	1	PNCA_ECOLI	P21369	escherichia
862	3	50.0	203	1	PYL2_METAC	P58863	methanosarc	935	3	50.0	213	1	STR5_MOUSE	Q9epq7	mus musculu
863	3	50.0	203	1	RR22_HUMAN	Q92737	homo sapien	936	3	50.0	213	1	TRMB_SYNEL	Q8dhn6	synechococc
864	3	50.0	204	1	ABP4_MAIZE	P33488	zea mays (m	937	3	50.0	213	1	TRPF_ACICA	P16923	acinetobact
865	3	50.0	204	1	BACR_HALHM	P33969	halobacteri	938	3	50.0	213	1	VE4_HPv65	Q07873	human papil
866	3	50.0	204	1	FTHC_SCHPO	Q9p7w2	schizosacch	939	3	50.0	214	1	ATP6_ALBCO	P48893	albinaria c
867	3	50.0	204	1	HIS2_YERPE	Q8zfy1	yersinia pe	940	3	50.0	214	1	GALI_CANMA	P56599	candida mal
868	3	50.0	204	1	NU6M_CHOCH	P48924	chondrus cr	941	3	50.0	214	1	NODA_METNO	Q9f0c9	methylobact
869	3	50.0	204	1	SC7_SCHCO	P35794	schizophyll	942	3	50.0	214	1	NODB_RHIGA	P50354	rhizobium g
870	3	50.0	204	1	SLI2_RALSO	O30920	ralstonia s	943	3	50.0	214	1	PPCT_HUMAN	Q9ukl6	homo sapien
871	3	50.0	204	1	THIE_RHIET	Q34294	rhizobium e	944	3	50.0	214	1	PPCT_MOUSE	P53808	mus musculu
872	3	50.0	204	1	UNG_HSVBC	P53764	bovine herp	945	3	50.0	214	1	PPCT_RAT	P53809	rattus norv
873	3	50.0	204	1	YT16_CAEEL	Q10919	caenorhabdi	946	3	50.0	214	1	RL1_METKA	Q8tx51	methanopyru
874	3	50.0	205	1	CN7A_SCHPO	Q9uuJ7	schizosacch	947	3	50.0	214	1	SC14_SCHCO	P35795	schizophyll
875	3	50.0	205	1	RNH2_CHLTE	Q8kaa5	chlorobium	948	3	50.0	214	1	TALI_LISIN	Q927a3	listeria in
876	3	50.0	205	1	TRPF_THEMEA	Q56320	thermotoga	949	3	50.0	214	1	TALI_LISMO	Q8y3t8	listeria mo
877	3	50.0	206	1	BACH_HALHM	P33970	halobacteri	950	3	50.0	214	1	ULDO_HCMVA	P16772	human cytom
878	3	50.0	206	1	EFA4_MOUSE	O08542	mus musculu	951	3	50.0	214	1	Y117_MYCGE	P47363	mycoplasma
879	3	50.0	206	1	GSPJ_ERWCH	P24689	erwinia chr	952	3	50.0	215	1	CCMB_PARDE	P52219	paracoccu
880	3	50.0	206	1	RNH2_METTH	O27102	methanobact	953	3	50.0	215	1	HIS5_STRAW	Q82aa2	streptomyce
881	3	50.0	206	1	TPIS_AEDTO	P92119	aedes togoi	954	3	50.0	215	1	IF4E_APLCA	O77210	aplysia cal
882	3	50.0	206	1	TPIS_ANOME	P91895	anopheles m	955	3	50.0	215	1	NODB_RHILT	P04676	rhizobium l
883	3	50.0	206	1	TPIS_CULPI	P91919	culex pipie	956	3	50.0	215	1	NODB_RHISN	P50355	rhizobium s
884	3	50.0	206	1	TRPF_PSEPK	Q881e0	pseudomonas	957	3	50.0	215	1	PTH_DEIRA	Q9rrw3	deinococcu
885	3	50.0	206	1	UREG_UREPA	Q56561	ureaplasma	958	3	50.0	215	1	SFT2_YEAST	P38166	saccharomyc
886	3	50.0	206	1	Y930_HAEIN	P44077	haemophilus	959	3	50.0	215	1	Y034_NPVAC	P21287	autographa
887	3	50.0	206	1	YG2C_YEAST	P53058	saccharomyc	960	3	50.0	215	1	Y233_XYLFA	Q9pgt5	xylella fas
888	3	50.0	207	1	LEXA_AERHY	Q44069	aeromonas h	961	3	50.0	215	1	Y267_BUCAI	P57355	buchnera ap
889	3	50.0	208	1	PSD_METAC	Q8tuf2	methanosarc	962	3	50.0	216	1	COX2_CALGO	P50661	callimico g
890	3	50.0	208	1	RS8_CAEEL	P48156	caenorhabdi	963	3	50.0	216	1	CSGD_ECOLI	P52106	escherichia
891	3	50.0	208	1	TESA_ECOLI	P29679	escherichia	964	3	50.0	216	1	CSGD_SALTY	O54294	salmonella
892	3	50.0	208	1	Y755_HALN1	Q9hrc8	halobacteri	965	3	50.0	216	1	DEFA_STRCO	Q9k4a0	streptomyce
893	3	50.0	208	1	YK69_CAEEL	P34347	caenorhabdi	966	3	50.0	216	1	INAA_ECOLI	P27294	escherichia
894	3	50.0	209	1	CXX1_HUMAN	O15255	homo sapien	967	3	50.0	216	1	KPT2_ARCFU	O28719	archaeoglob
895	3	50.0	209	1	RS3_THEMEA	P46772	thermotoga	968	3	50.0	216	1	NODB_RHILV	P04339	rhizobium l
896	3	50.0	209	1	ULB8_HCMVA	P16834	human cytom	969	3	50.0	216	1	PGSA_TREPA	O66076	treponema p
897	3	50.0	210	1	ENGB_PSEPK	Q88rk5	pseudomonas	970	3	50.0	216	1	PIM1_ARCFU	O30199	archaeoglob
898	3	50.0	210	1	FTSQ_AGRFU	O30990	agrobacteri	971	3	50.0	216	1	RGSJ_MOUSE	Q9cx84	mus musculu
899	3	50.0	210	1	NIP3_CAEEL	Q09969	caenorhabdi	972	3	50.0	216	1	RGSJ_RAT	O70521	rattus norv
900	3	50.0	210	1	NODA_BRAEL	P50326	bradyrhizob	973	3	50.0	216	1	SGAH_ECOLI	P39304	escherichia
901	3	50.0	210	1	NODA_BRAJA	Q9amz0	bradyrhizob	974	3	50.0	216	1	Y192_XYLFT	Q87ev6	xylella fas
902	3	50.0	210	1	NODA_BRASN	P50347	bradyrhizob	975	3	50.0	216	1	Y458_METJA	Q57900	methanococc
903	3	50.0	210	1	NODA_BRASP	P04674	bradyrhizob	976	3	50.0	217	1	FLA1_METJA	Q58301	methanococc
904	3	50.0	210	1	RGSH_CHICK	Q9pwa0	gallus gall	977	3	50.0	217	1	NODB_RHIME	P02963	rhizobium m
905	3	50.0	210	1	XYNA_BACST	P45705	bacillus st	978	3	50.0	217	1	O2A5_HUMAN	Q96r48	homo sapien
906	3	50.0	210	1	YAC9_MAIZE	P03936	zea mays (m	979	3	50.0	217	1	RGSJ_HUMAN	P49795	homo sapien
907	3	50.0	210	1	YO43_HALN1	Q9hnh2	halobacteri	980	3	50.0	217	1	TAL_BRUME	Q8yj42	brucella me
908	3	50.0	210	1	YQS3_CAEEL	Q09311	caenorhabdi	981	3	50.0	217	1	TAL_BRUSU	Q8fyq9	brucella su
909	3	50.0	210	1	YRBL_ECOLI	P46021	escherichia	982	3	50.0	217	1	TRPF_CANGA	P50857	candida gla

910	3	50.0	211	1	NDK5_MOUSE	Q99mh5	mus musculu
911	3	50.0	211	1	THIE_ECO57	P27764	pseudomonas
912	3	50.0	211	1	THIE_ECOL6	Q98pk6	mycoplasma
913	3	50.0	211	1	THIE_ECOLI	P05754	saccharomyc
914	3	50.0	211	1	THIE_SALTI	P44603	haemophilus
915	3	50.0	211	1	THIE_SALTY	P73888	synechocyst
916	3	50.0	211	1	TRPF_PSEAE	Q57213	haemophilus
917	3	50.0	211	1	TX10_HUMAN	P05221	xenopus lae
918	3	50.0	211	1	YNQ8_CAEEL	O51123	borrelia bu
919	3	50.0	211	1	ZFP5_ARATH	Q8fnf8	corynebacte
920	3	50.0	212	1	GRPE_LEPIN	P13689	zea mays (m
921	3	50.0	212	1	KTHY_SYNY3	Q9cg29	lactococcus
922	3	50.0	212	1	NDK5_HUMAN	O68854	rhizobium m
923	3	50.0	212	1	PPIC_HUMAN	Q45335	brucella ov
924	3	50.0	212	1	PYEL_HALN1	P16740	human cytom
925	3	50.0	212	1	TAL_BACSU	P26881	legionella
926	3	50.0	212	1	USO1_HCMVA	Q9pjp9	chlamydia m
927	3	50.0	213	1	CPCF_SYNEL	Q99m38	mus musculu
928	3	50.0	213	1	HIS1_BACSU	Q99m38	mus musculu
929	3	50.0	213	1	OM25_BRUAB	Q99m38	mus musculu
930	3	50.0	213	1	OM25_BRUCA	Q99m38	mus musculu
931	3	50.0	213	1	OM25_BRUME	Q99m38	mus musculu
932	3	50.0	213	1	OM25_BRUNE	Q99m38	mus musculu
933	3	50.0	213	1	OM25_BRUSU	Q99m38	mus musculu
934	3	50.0	213	1	PNCA_ECOLI	Q99m38	mus musculu
935	3	50.0	213	1	STR5_MOUSE	Q99m38	mus musculu
936	3	50.0	213	1	TRMB_SYNEL	Q99m38	mus musculu
937	3	50.0	213	1	TRPF_ACICA	Q99m38	mus musculu
938	3	50.0	213	1	VE4_HP65	Q99m38	mus musculu
939	3	50.0	214	1	ATP6_ALBCO	Q99m38	mus musculu
940	3	50.0	214	1	GAL1_CANMA	Q99m38	mus musculu
941	3	50.0	214	1	NODA_METNO	Q99m38	mus musculu
942	3	50.0	214	1	NODB_RHIGA	Q99m38	mus musculu
943	3	50.0	214	1	PPCT_HUMAN	Q99m38	mus musculu
944	3	50.0	214	1	PPCT_MOUSE	Q99m38	mus musculu
945	3	50.0	214	1	PPCT_RAT	Q99m38	mus musculu
946	3	50.0	214	1	RL1_METKA	Q99m38	mus musculu
947	3	50.0	214	1	SC14_SCHCO	Q99m38	mus musculu
948	3	50.0	214	1	TAL1_LISIN	Q99m38	mus musculu
949	3	50.0	214	1	TAL1_LISMO	Q99m38	mus musculu
950	3	50.0	214	1	ULD0_HCMVA	Q99m38	mus musculu
951	3	50.0	214	1	Y117_MYCGE	Q99m38	mus musculu
952	3	50.0	215	1	CCMB_PARDE	Q99m38	mus musculu
953	3	50.0	215	1	HIS5_STRAW	Q99m38	mus musculu
954	3	50.0	215	1	IF4E_APLCA	Q99m38	mus musculu
955	3	50.0	215	1	NODB_RHILT	Q99m38	mus musculu
956	3	50.0	215	1	NODB_RHISN	Q99m38	mus musculu
957	3	50.0	215	1	PTH_DEIRA	Q99m38	mus musculu
958	3	50.0	215	1	SFT2_YEAST	Q99m38	mus musculu
959	3	50.0	215	1	Y034_NPVAC	Q99m38	mus musculu
960	3	50.0	215	1	Y233_XYLFA	Q99m38	mus musculu
961	3	50.0	215	1	Y267_BUCAI	Q99m38	mus musculu
962	3	50.0	216	1	COX2_CALGO	Q99m38	mus musculu
963	3	50.0	216	1	CSGD_ECOLI	Q99m38	mus musculu
964	3	50.0	216	1	CSGD_SALTY	Q99m38	mus musculu
965	3	50.0	216	1	DEF4_STRCO	Q99m38	mus musculu
966	3	50.0	216	1	INAA_ECOLI	Q99m38	mus musculu
967	3	50.0	216	1	KPT2_ARCFU	Q99m38	mus musculu
968	3	50.0	216	1	NODB_RHILV	Q99m38	mus musculu
969	3	50.0	216	1	PGSA_TREPA	Q99m38	mus musculu
970	3	50.0	216	1	PIM1_ARCFU	Q99m38	mus musculu
971	3	50.0	216	1	RGSJ_MOUSE	Q99m38	mus musculu
972	3	50.0	216	1	RGSJ_RAT	Q99m38	mus musculu
973	3	50.0	216	1	SGAH_ECOLI	Q99m38	mus musculu
974	3	50.0	216	1	Y192_XYLFT	Q99m38	mus musculu
975	3	50.0	216	1	Y458_METJA	Q99m38	mus musculu
976	3	50.0	217	1	FLA1_METJA	Q99m38	mus musculu
977	3	50.0	217	1	NODB_RHIME	Q99m38	mus musculu
978	3	50.0	217	1	O2A5_HUMAN	Q99m38	mus musculu
979	3	50.0	217	1	RGSJ_HUMAN	Q99m38	mus musculu
980	3	50.0	217	1	TAL_BRUME	Q99m38	mus musculu
981	3	50.0	217	1	TAL_BRUSU	Q99m38	mus musculu
982	3	50.0	217	1	TRPF_CANGA	Q99m38	mus musculu


```
983 3 50.0 217 1 UNG_PSEDE
984 3 50.0 217 1 UNG_STR3
985 3 50.0 217 1 UNG_STRMU
986 3 50.0 217 1 UREF_SYNY3
987 3 50.0 218 1 A4GT_PONPY
988 3 50.0 218 1 KAD_BORPE
989 3 50.0 218 1 MOBA_AGR5
990 3 50.0 218 1 NIPL_MOUSE
991 3 50.0 218 1 RS5_AERPE
992 3 50.0 218 1 TAL_RHILO
993 3 50.0 218 1 UL71_EBV
994 3 50.0 218 1 Y522_HAEIN
995 3 50.0 218 1 YBOF_SCHPO
996 3 50.0 219 1 CYB6_HETTR
997 3 50.0 219 1 END3_BACSU
998 3 50.0 219 1 GLNP_ECOLI
999 3 50.0 219 1 NIPL_HUMAN
1000 3 50.0 219 1 NODB_BRAEL
```

ALIGNMENTS

```
RESULT 1
NRAM_IADBU
ID_NRAM_IADBU STANDARD; PRT; 470 AA.
AC Q07570;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Burjatia/652/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06572; AAA43365.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
```

```
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51989 MW; D1A6F07460F6F8AD CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 2
NRAM_IADCH
ID_NRAM_IADCH STANDARD; PRT; 470 AA.
AC Q07571;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06573; AAA43367.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 39 88 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
```



```
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 169AB89FBE8006DC CRC64;

Query Match      83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 3
NRAM_IADH2
ID_NRAM_IADH2 STANDARD; PRT; 470 AA.
AC Q07572;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06574; AAA43372.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52015 MW; E1C1D3E2C650B93C CRC64;
```

```
Query Match      83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 4
NRAM_IADM2
ID_NRAM_IADM2 STANDARD; PRT; 470 AA.
AC Q07573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06575; AAA43404.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52146 MW; 30F5F9FE364C1F49 CRC64;

Query Match      83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
QY      1 ADWSW 5
Db      453 ADWSW 457

RESULT 5
NRAM_IADU3
ID_NRAM_IADU3      STANDARD;      PRT;      470 AA.
AC      Q07599;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neuraminidase (EC 3.2.1.18).
GN      NA.
OS      Influenza A virus (strain A/Duck/Ukraine/1/63).
OC      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC      Influenza A viruses; Influenzavirus A.
OX      NCBI_TaxID=11374;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93212520; PubMed=8460490;
RA      Saito T., Kawaoka Y., Webster R.G.;
RT      "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT      viruses.";
RL      Virology 193:868-876(1993).
CC      -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC      chains of the host cell surface proteins and from the viral
CC      envelope. Such a reaction prevents self-aggregation and facilitate
CC      the mobility of the virus to and from the site of infection.
CC      -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC      alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC      oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC      synthetic substrates.
CC      -!- SUBUNIT: Homotetramer.
CC      -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC      spike on the surface of the virion.
CC      -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L06576; AAA16234.1; -.
DR      HSSP; P06820; 2BAT.
DR      InterPro; IPR001860; Glyco_hydro_34.
DR      Pfam; PF00064; neur; 1.
DR      ProDom; PD000431; Glyco_hydro_34; 1.
DR      Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
DR      TRANSMEM 7 37 ANCHOR (BY SIMILARITY).
FT      DOMAIN 38 88 HYPERVARIABLE STALK REGION.
FT      DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT      ACT_SITE 273 275 PROBABLE.
FT      ACT_SITE 275 275 PROBABLE.
FT      CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

Query Match      83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      453 ADWSW 457

RESULT 6
NRAM_IAGFN
ID_NRAM_IAGFN      STANDARD;      PRT;      470 AA.
AC      Q07574;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neuraminidase (EC 3.2.1.18).
GN      NA.
OS      Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC      Influenza A viruses; Influenzavirus A.
OX      NCBI_TaxID=38963;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93212520; PubMed=8460490;
RA      Saito T., Kawaoka Y., Webster R.G.;
RT      "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT      viruses.";
RL      Virology 193:868-876(1993).
CC      -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC      chains of the host cell surface proteins and from the viral
CC      envelope. Such a reaction prevents self-aggregation and facilitate
CC      the mobility of the virus to and from the site of infection.
CC      -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC      alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC      oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC      synthetic substrates.
CC      -!- SUBUNIT: Homotetramer.
CC      -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC      spike on the surface of the virion.
CC      -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L06584; AAA43428.1; -.
DR      HSSP; P06820; 2BAT.
DR      InterPro; IPR001860; Glyco_hydro_34.
DR      Pfam; PF00064; neur; 1.
DR      ProDom; PD000431; Glyco_hydro_34; 1.
DR      Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
DR      TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT      DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT      DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT      ACT_SITE 273 275 BY SIMILARITY.
FT      ACT_SITE 275 275 BY SIMILARITY.
FT      CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;

Query Match      83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      453 ADWSW 457

RESULT 7
NRAM_IAHGD
ID_NRAM_IAHGD      STANDARD;      PRT;      470 AA.
```


AC Q07577;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Herring gull/DE/677/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38964;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06585; AAA43368.1; --.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 8
NRAM_IAHJI
ID_NRAM_IAHJI STANDARD; PRT; 470 AA.
AC Q07578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Equine/Jilllin/1/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06579; AAA43374.1; --.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 9
NRAM_IAMAE
ID_NRAM_IAMAE STANDARD; PRT; 470 AA.
AC Q07583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;


```
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38965;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06586; AAA43369.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E11F2765 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 10
NRAM_IATKL STANDARD; PRT; 470 AA.
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06588; AAA43410.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; DE573742ABFF1E6B CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 11
MRJ5_APIME STANDARD; PRT; 598 AA.
ID MRJ5_APIME
AC O97432;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=99373663; PubMed=10441680;
RA Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.;
```


RT "The family of major royal jelly proteins and its evolution.";
RL J. Mol. Evol. 49:290-297(1999).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
CC HONEYBEE QUEEN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
CC -1- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
CC the nurse honey bee.
CC -1- SIMILARITY: Belongs to the major royal jelly protein family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF004842; AAD01205.1; -.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal; Repeat; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C77E7ACDF63 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 113 DWSWA 117

RESULT 12
LCCB_LEUME
ID_LCCB_LEUME STANDARD; PRT; 31 AA.
AC P81052;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Bacteriocin leucocin B.
OS Leuconostoc mesenteroides.
OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
OX NCBI_TaxID=1245;
RN [1]
RP SEQUENCE.
RC STRAIN-TA33a;
RX MEDLINE=98274743; PubMed=9611809;
RA Papathanasopoulos M.A., Dykes G.A., Revol-Junelles A.-M., Delfour A.,
RA von Holy A., Hastings J.W.;
RT "Sequence and structural relationships of leucocins A-, B- and
RT C-TA33a from Leuconostoc mesenteroides TA33a.";
RL Microbiology 144:1343-1348(1998).
CC -1- FUNCTION: Inhibits a wide spectrum of lactic acid bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Bacteriocin; Antibiotic.
SQ SEQUENCE 31 AA; 3466 MW; 7C8DD9C387D34D55 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6

Db |||||
6 WSWA 9
RESULT 13
TXD3_PARLU
ID_TXD3_PARLU STANDARD; PRT; 36 AA.
AC P83258;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-palutoxin IT3 (Delta-palutrit3).
OS Paracoelotes luctuosus (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Amaurobiidae; Paracoelotes.
OX NCBI_TaxID=185217;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20428467; PubMed=10971590;
RA Corzo G., Escoubas P., Stankiewicz M., Pelhate M., Kristensen C.P.,
RA Nakajima T.;
RT "Isolation, synthesis and pharmacological characterization of
RT delta-palutoxins IT, novel insecticidal toxins from the spider
RT Paracoelotes luctuosus (Amaurobiidae).";
RL Eur. J. Biochem. 267:5783-5795(2000).
CC -1- FUNCTION: Potent activity against S.litura larvae.
CC -1- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels. This toxin is active only on insects
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=3926.2; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the mu-agatoxin family.
CC GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0019871; F:sodium channel inhibitor activity; IDA.
DR GO; GO:0015070; F:toxin activity; IDA.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
FT DISULFID 3 19 BY SIMILARITY.
FT DISULFID 10 24 BY SIMILARITY.
FT DISULFID 18 34 BY SIMILARITY.
FT DISULFID 26 32 BY SIMILARITY.
SQ SEQUENCE 36 AA; 3934 MW; 9CDFDAD043A19804 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 11 ADWS 14

RESULT 14
TXD1_PARLU
ID_TXD1_PARLU STANDARD; PRT; 37 AA.
AC P83256;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-palutoxin IT1 (Delta-palutrit1).
OS Paracoelotes luctuosus (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Amaurobiidae; Paracoelotes.
OX NCBI_TaxID=185217;
RN [1]
RP SEQUENCE, SYNTHESIS, FUNCTION, DISULFIDE BONDS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20428467; PubMed=10971590;
RA Corzo G., Escoubas P., Stankiewicz M., Pelhate M., Kristensen C.P.,
RA Nakajima T.;
RT "Isolation, synthesis and pharmacological characterization of
RT delta-palutoxins IT, novel insecticidal toxins from the spider


```
RT Paracaelotes luctuosus (Amaurobiidae).";
RL Eur. J. Biochem. 267:5793-5795(2000).
CC -|- FUNCTION: Potent activity against S.litura larvae.
CC -|- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels. This toxin is active only on insects.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -|- MASS SPECTROMETRY: MW=4037.9; METHOD=MALDI.
CC -|- SIMILARITY: Belongs to the mu-agatoxin family.
CC PIR; A59401; A59401.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0019871; F:sodium channel inhibitor activity; IDA.
DR GO; GO:0015070; F:toxin activity; IDA.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Amidation;
KW Sodium channel inhibitor.
FT DISULFID 2 18
FT DISULFID 9 23
FT DISULFID 17 33
FT DISULFID 25 31
FT MOD_RES 37 37
FT SEQUENCE 37 AA; 4046 MW; E019DABCC25BC11E CRC64;
SQ
Query Match 66.7%; Score 4; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 10 ADWS 13

RESULT 15
ACYP MYCTU
ID ACYP_MYCTU STANDARD; PRT; 93 AA.
AC P56543;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative acylphosphatase (EC 3.6.1.7) (Acylphosphate
phosphohydrolase).
GN ACYP OR RV2922.1C OR MT2991 OR MTCY338.11BC OR MB2947C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=2206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).

[3]
RN SEQUENCE FROM N.A.
RP SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
RN [4]
RP IDENTIFICATION.
RC SPECIES=M.tuberculosis;
RA Bairoch A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: An acyl phosphate + H(2)O = a fatty acid anion
CC + phosphate.
CC -|- SIMILARITY: Belongs to the acylphosphatase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z74697; -, NOT ANNOTATED_CDS.
CC EMBL; AE007121; AAK47318.1; -.
CC EMBL; BX248344; CAD96634.1; -.
CC TIGR; MT2991; -.
CC Tuberculist; RV2922.1c; -.
CC InterPro; IPR001792; Acylphosphatase.
CC Pfam; PF00708; Acylphosphatase; 1.
CC ProDom; PD001884; Acylphosphatase; 1.
CC PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
CC PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
KW Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 93 AA; 10206 MW; 63A90ED2D780DDEB CRC64;

Query Match 66.7%; Score 4; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 78 ADWS 81

RESULT 16
Y451_BUCAP
ID Y451_BUCAP STANDARD; PRT; 114 AA.
AC Q8K998;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein BUSG451.
GN BUSG451.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Werngreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -|- SIMILARITY: BELONGS TO THE DSCR/DSVC FAMILY. STRONG, TO
CC E.COLI YCCK OR H.INFLUENZAE HI1371.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
```


CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE014121; AAM67994.1; -.
DR InterPro; IPR007453; Dsrc.
DR Pfam; PF04358; Dsrc; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 114 AA; 13332 MW; 775C9CF21A9AB41A CRC64;

Query Match 66.7%; Score 4; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 26 ADWS 29

RESULT 17

YRDN_BACSU STANDARD; PRT; 128 AA.
AC P94502; O08187;
DT 15-JUL-1998 (Rel. 36, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable tautomerase yrdN (EC 5.3.2.-).
GN YRDN OR BSU26660.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / SMY;
RX MEDLINE=97175526; PubMed=9023181;
RA Belitsky B.R., Sonenshein A.L.;
RT "Altered transcription activation specificity of a mutant form of
RT Bacillus subtilis GltR, a LysR family member."
RL J. Bacteriol. 179:1035-1043(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=9308178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors SigV and SigZ."
RL Microbiology 143:2939-2943(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borribs R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kabahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maul C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terptrata P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -I- FUNCTION: PUTATIVE TARGET OF GLTR.
CC -I- SIMILARITY: Belongs to the tautomerase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U79494; AAB47964.1; -.
DR EMBL; U93876; AAB80906.1; -.
DR EMBL; Z99117; CAB14607.1; -.
DR PIR; E69973; E69973.
DR Subtilist; BG12287; yrdN.
DR InterPro; IPR004370; Taut.
DR Pfam; PF01361; Tautomerase; 1.
KW Isomerase; Complete proteome.
FT INIT_MET 0 0 BY SIMILARITY.
FT ACT_SITE 1 1 CATALYTIC BASE (BY SIMILARITY).
SQ SEQUENCE 128 AA; 14550 MW; 6D148A7184E720EF CRC64;

Query Match 66.7%; Score 4; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 112 ADWS 115

RESULT 18
VG29_BPMD2 STANDARD; PRT; 147 AA.
ID VG29 BPMD2
AC O64223;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Gene 29 protein (GP29).
GN 29.
OS Mycobacteriophage D29.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=28369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: implications for phage
RT evolution."
RL J. Mol. Biol. 279:143-164(1998).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----


```
CC -----
DR EMBL; AF022214; AAC18470.1; -.
DR PIR; C72803; C72803.
SQ SEQUENCE 147 AA; 16982 MW; 54B877CBEDA82C33 CRC64;

Query Match      66.7%; Score 4; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      ||||
      40 ADWS 43

RESULT 19
VG29_BPML5
ID_VG29_BPML5 STANDARD; PRT; 147 AA.
AC Q05236;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Gene 29 protein (GP29).
GN 29.
OS Mycobacteriophage L5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC L5-like viruses.
OX NCBI_TaxID=31757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211282; PubMed=8459766;
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC SEQUENCE 147 AA; 16900 MW; 4DC675311403D3B9 CRC64;

Query Match      66.7%; Score 4; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      ||||
      40 ADWS 43

RESULT 20
YB19_PSEPK
ID_YB19_PSEPK STANDARD; PRT; 160 AA.
AC Q88NT5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0225 protein PP1119.
GN PP1119.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
```

```
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
CC -!- SIMILARITY: Belongs to the UPF0225 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC SEQUENCE 160 AA; 17414 MW; 1213A502E31732B6 CRC64;

DR EMBL; AE016778; AAN66744.1; -.
DR TIGR; PP1119; -.
DR HAMAP; MF 00612; -; 1.
DR InterPro; IPR004027; SEC_C_motif.
DR Pfam; PF02810; SEC-C; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 160 AA; 17414 MW; 1213A502E31732B6 CRC64;

Query Match      66.7%; Score 4; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      ||||
      68 ADWS 71

RESULT 21
CX41_MOUSE
ID_CX41_MOUSE STANDARD; PRT; 169 AA.
AC P19783;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor
DE (EC 1.9.3.1) (COX IV-1) (Cytochrome c oxidase polypeptide IV).
GN COX4I1 OR COX4A OR COX4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Heart;
RX MEDLINE=91057158; PubMed=2173832;
RA Groseman L.I., Akamatsu M.;
RT "Nucleotide sequence of a mouse cDNA for subunit IV of cytochrome c
oxidase.";
RL Nucleic Acids Res. 18:6454-6454(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91378465; PubMed=1654830;
RA Carter R.S., Avadhani N.G.;
RT "Cloning and characterization of the mouse cytochrome c oxidase
subunit IV gene.";
RL Arch. Biochem. Biophys. 288:97-106(1991).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
```


CC -!- SIMILARITY: Belongs to the cytochrome c oxidase IV family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M37831; AAB02139.1; -.
DR EMBL; M58034; AAB02139.1; JOINED.
DR EMBL; M37829; AAB02140.1; -.
DR EMBL; X54691; CAA38507.1; -.
DR PIR; S12142; S12142.
DR MGD; MGI:88473; Cox4i1.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR InterPro; IPR004203; COX4.
DR Pfam; PF02936; COX4; 1.
KW Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide.
FT TRANSIT 1 22 MITOCHONDRION.
FT CHAIN 23 169 CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM
FT 1.
FT CONFLICT 34 34 A -> R (IN REF. 1).
FT CONFLICT 71 71 S -> N (IN REF. 1).
FT CONFLICT 140 141 MQ -> IE (IN REF. 1; AAB02139 AND 2).
SQ SEQUENCE 169 AA; 19530 MW; D30B1DBBE14FDDEA CRC64;

Query Match 66.7%; Score 4; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 68 ADWS 71

RESULT 22
CX41_RAT
ID_CX41_RAT STANDARD; PRT; 169 AA.
AC P10888;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor
DE (EC 1.9.3.1) (COX IV-1) (Cytochrome c oxidase polypeptide IV).
GN COX4i1 OR COX4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=89240039; PubMed=2541414;
RA Goto Y., Amuro N., Okazaki T.;
RT "Nucleotide sequence of cDNA for rat brain and liver cytochrome c
RT oxidase subunit IV.";
RL Nucleic Acids Res. 17:2851-2851(1989).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=89296488; PubMed=2544859;
RA Gopalan G., Droste M., Kadenbach B.;
RT "Nucleotide sequence of cDNA encoding subunit IV of cytochrome c
RT oxidase from fetal rat liver.";
RL Nucleic Acids Res. 17:4376-4376(1989).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=90237079; PubMed=2159010;
RA Yamada M., Amuro N., Goto Y., Okazaki T.;
RT "Structural organization of the rat cytochrome c oxidase subunit IV
RT gene.";

RL J. Biol. Chem. 265:7687-7692(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90326528; PubMed=2165254;
RA Amuro N., Yamada M., Goto Y., Okazaki T.;
RT "Complete nucleotide sequence of the gene encoding rat cytochrome c
RT oxidase subunit IV.";
RL Nucleic Acids Res. 18:3992-3992(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=91067442; PubMed=2174541;
RA Virbasius J.V., Scarpulla R.C.;
RT "The rat cytochrome c oxidase subunit IV gene family: tissue-specific
RT and hormonal differences in subunit IV and cytochrome c mRNA
RT expression.";
RL Nucleic Acids Res. 18:6581-6586(1990).
RN [6]
RP SEQUENCE OF 23-32.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halanek W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase IV family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X14209; CAA32426.1; -.
DR EMBL; X15029; CAA33133.1; -.
DR EMBL; J05425; AAA40949.1; -.
DR EMBL; X54081; CAA38018.1; -.
DR PIR; A35209; A35209.
DR InterPro; IPR004203; COX4.
DR Pfam; PF02936; COX4; 1.
KW Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide.
FT TRANSIT 1 22 MITOCHONDRION.
FT CHAIN 23 169 CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM
FT 1.
SQ SEQUENCE 169 AA; 19514 MW; F0187C76B7A1A9FE CRC64;

Query Match 66.7%; Score 4; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 68 ADWS 71

RESULT 23
RL18_HALN1
ID_RL18_HALN1 STANDARD; PRT; 182 AA.
AC P50562; Q9HPB5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L18P (HSa118).
GN RPL18P OR VNGI714G.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and

OS Halobacterium salinarium.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091, 2242;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN [2]
RP SEQUENCE OF 1-23.
RC SPECIES=H.salinarium; STRAIN=DSM 3754;
RX MEDLINE=94229075; PubMed=8174557;
RA McDougall J., Wittmann-Liebold B.;
RT "Comparative analysis of the protein components from 5S rRNA.protein
RT complexes of halophilic archaeobacteria.";
RL Eur. J. Biochem. 221:779-785(1994).
CC -!- SIMILARITY: Belongs to the L18P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE005077; AAG19955.1; -.
DR PIR; G84323; G84323.
DR InterPro; IPR005484; Ribosomal_L18p.
DR Pfam; PF00861; Ribosomal_L18p; 1.
KW Ribosomal protein; Complete proteome.
FT INIT MET 0
SQ SEQUENCE 182 AA; 19680 MW; 1607FD9C5243288B CRC64;

Query Match 66.7%; Score 4; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 137 ADWS 140

RESULT 24
YE21_AQUAE
ID YE21_AQUAE STANDARD; PRT; 197 AA.
AC O67415;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1421.
GN AQ_1421.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex

RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- SIMILARITY: Belongs to the UPF0033 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000739; AAC07381.1; -.
DR PIR; E70423; E70423.
DR InterPro; IPR001455; UPF0033.
DR Pfam; PF01206; UPF0033; 1.
DR PROSITE; PS01148; UPF0033; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 197 AA; 22604 MW; 3E8E5E9147C11DF2 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 51 WSWA 54

RESULT 25
HAM1_STRPN
ID HAM1_STRPN STANDARD; PRT; 200 AA.
AC Q97NX3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE HAM1 protein homolog.
GN SP1880 OR SPR1695.
OS Streptococcus pneumoniae, and
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313, 171101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-255 / R6;
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).


```
CC -!- SIMILARITY: Belongs to the HAM1 NTPase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE007478; AAK75952.1; -.
DR EMBL; AE008534; AAL00498.1; ALT_INIT.
DR PIR; G95219; G95219.
DR TIGR; SP1880; -.
DR HAMAP; MF 01405; -; 1.
DR InterPro; IPR002637; Ham1p_like.
DR Pfam; PF01725; Ham1p_like; 1.
DR ProDom; PD004952; Ham1p_like; 1.
DR TIGRFAMs; TIGR00042; TIGR00042; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 200 AA; 22041 MW; 991DAC2C847D31A8 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 135 ADWS 138

RESULT 26
TATB_XANAC STANDARD; PRT; 208 AA.
AC Q8PEX3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sec-independent protein translocase protein tatB homolog.
GN TATB OR XAC4217.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463 (2002).
CC -!- FUNCTION: Required for correct localization of precursor proteins
CC bearing signal peptides with the twin arginine conserved motif
CC S/T-R-X-F-L-K. This sec-independent pathway is termed TAT for
CC twin-arginine translocation system. This system mainly transports
CC proteins with bound cofactors that require folding prior to export
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Inner membrane-bound (Probable).
```

```
CC -!- SIMILARITY: Belongs to the tatB family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE012074; AAM39052.1; -.
DR HAMAP; MF 00237; -; 1.
DR InterPro; IPR003369; MttA_Hcf106.
DR InterPro; IPR003998; TatB.
DR Pfam; PF02416; MttA_Hcf106; 1.
DR PRINTS; PR01506; TATBPROTEIN.
DR TIGRFAMs; TIGR01410; tatB; 1.
KW Transport; Protein transport; Translocation; Transmembrane;
KW Inner membrane; Complete proteome.
FT TRANSMEM 1 21 POTENTIAL.
SQ SEQUENCE 208 AA; 21971 MW; A9431BD2F2BE84F6 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 117 ADWS 120

RESULT 27
VNCN_PAVBO STANDARD; PRT; 213 AA.
ID VNCN_PAVBO
AC P07295;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Probable noncapsid protein NP1.
OS Bovine parvovirus (BPV).
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10784;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87061184; PubMed=3783814;
RA Chen K.C., Shull B.C., Moses E.A., Lederman M., Stout E.R.,
RA Bates R.C.;
RT "Complete nucleotide sequence and genome organization of bovine
RT parvovirus."
RL J. Virol. 60:1085-1097 (1986).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M14363; AAB59846.1; -.
DR PIR; B26104; UYPVP1.
KW Noncapsid protein.
SQ SEQUENCE 213 AA; 24834 MW; 768CB1E8F77C2626 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 21 ADWS 24
```



```
RESULT 28
RECO_PSESM
ID_RECO_PSESM STANDARD; PRT; 227 AA.
AC Q87XG3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA repair protein recO (Recombination protein O).
GN RECO OR PSPTO4215.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidse T., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H., Fedorova N., Tran B., Russell D., Berry K., Uetexback T.,
RA Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,
RA Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,
RA Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
RA White O., Fraser C.M., Collmer A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -!- FUNCTION: Involved in DNA repair and recF pathway recombination
CC (By similarity).
CC -!- SIMILARITY: Belongs to the recO family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF016871; AA057671.1; -.
CC TIGR; PSPTO4215; -.
CC HAMAP; MF_00201; -.
CC InterPro; IPR003717; RecO.
CC Pfam; PF02565; RecO; 1.
CC DNA repair; DNA recombination; Complete proteome.
CC SEQUENCE 227 AA; 24930 MW; 43A1D9D6AE6BFCFC CRC64;

Query Match 66.7%; Score 4; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 190 ADWS 193

RESULT 29
RECO_PSEAE
ID_RECO_PSEAE STANDARD; PRT; 233 AA.
AC Q9XCX7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA repair protein recO (Recombination protein O).
GN RECO OR PA0772.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=PAK;
RX MEDLINE=99369891; PubMed=10438789;
RA Powell B.S., Peters H.K. III, Nakamura Y., Court D.L.;
RT "Cloning and analysis of the rnc-era-recO operon from Pseudomonas
RT aeruginosa.";
RN J. Bacteriol. 181:5111-5113(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Involved in DNA repair and recF pathway recombination
CC (By similarity).
CC -!- SIMILARITY: Belongs to the recO family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 196.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF123492; AAD40231.1; ALT_FRAME.
CC EMBL; AE004512; AAG04161.1; -.
CC PIR; G83548; G83548.
CC HAMAP; MF_00201; -.
CC InterPro; IPR003717; RecO.
CC Pfam; PF02565; RecO; 1.
CC DNA repair; DNA recombination; Complete proteome.
CC SEQUENCE 233 AA; 25498 MW; 67ABBE6BCDE2DC1A CRC64;

Query Match 66.7%; Score 4; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 190 ADWS 193

RESULT 30
UBIE_LISMO
ID_UBIE_LISMO STANDARD; PRT; 237 AA.
AC Q92A77;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Menquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
GN UBIE OR LMO1931 OR LIN2045.
OS Listeria monocytogenes, and
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639, 1642;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=L.monocytogenes, and L.innocua;
RC STRAIN=EGD-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
```


RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordtsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlutner T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlend J., Cossart P.;
RT "Comparative genomics of *Listeria species*.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Methyltransferase required for the conversion of
CC dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
CC S-adenosyl-L-homocysteine + menaquinol.
CC -1- PATHWAY: Menaquinone biosynthesis; last step.
CC -1- SIMILARITY: Belongs to the ubiE family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL591981; CAD00009.1; --
CC EMBL; AL596170; CAC97275.1; --
CC PIR; AC1316; AC1316.
CC PIR; AC1688; AC1688.
CC ListList; LIN02045; --
CC ListList; LMO01931; --
CC HAMAP; MF 01813; --; 1.
CC InterPro; IPR001601; Methyltransf.
CC InterPro; IPR000051; SAM bind.
CC InterPro; IPR004034; Ubi7men Metransf.
CC InterPro; IPR004033; UbiE/COQ5 Metrf.
CC Pfam; PF01209; Ubie_methyltran; 1.
CC PROSITE; PS01183; UBI1; 1.
CC PROSITE; PS01184; UBI2; FALSE NEG.
KW Menaquinone biosynthesis; Transferase; Methyltransferase;
KW Complete proteome.
SQ SEQUENCE 237 AA; 27330 MW; 3363669F83D9AC74 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 59 ADWS 62

RESULT 31
TAM_RHILO STANDARD; PRT; 256 AA.
ID TAM_RHILO STANDARD; PRT; 256 AA.
AC Q98K73;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trans-aconitate 2-methyltransferase (EC 2.1.1.144).
GN TAM OR MLL1606.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
CC -1- FUNCTION: Catalyzes the S-adenosylmethionine monomethyl
CC esterification of trans-aconitate (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + trans-aconitate = S-
CC adenosyl-L-homocysteine + (E)-3-(methoxycarbonyl)pent-2-enedioate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Tam
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP002997; BAB48941.1; --
CC HAMAP; MF 00560; --; 1.
CC InterPro; IPR000051; SAM bind.
KW Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 256 AA; 28539 MW; AAB7B101141B4608 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 2 ADWS 5

RESULT 32
YK09_RALSO STANDARD; PRT; 257 AA.
ID YK09_RALSO STANDARD; PRT; 257 AA.
AC Q8XXV4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0246 protein RSC2009.
GN RSC2009 OR RS03577.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.-C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";
RL Nature 415:497-502(2002).
CC -1- SIMILARITY: Belongs to the UPF0246 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL646067; CAD15711.1; --
CC HAMAP; MF 00652; --; 1.
CC InterPro; IPR005583; DUF328.
CC Pfam; PF03883; DUF328; 1.


```
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 28974 MW; 8E44372F7FFD7E3A CRC64;

Query Match 66.7%; Score 4; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 65 ADWS 68

RESULT 33
DET2_ARATH
ID DET2_ARATH STANDARD; PRT; 262 AA.
AC Q38944; Q9SH83;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable steroid reductase DET2 (EC 1.3.99.-).
GN DET2 OR AT2G38050 OR T8P21.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=96185496; PubMed=8602526;
RA Li J., Nagpal P., Vitart V., McMorris T.C., Chory J.;
RT "A role for brassinosteroids in light-dependent development of
Arabidopsis.";
RL Science 272:398-401(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome.";
RL Science 302:842-846(2003).
CC -!- FUNCTION: Probably involved in a reduction step in the
biosynthesis of the plant steroid, brassinolide. Defects in DET2
leads to defects in light-regulated development.
CC -!- PATHWAY: Brassinolide biosynthesis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
```

```
CC -!- SIMILARITY: Belongs to the steroid 5-alpha reductase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U53860; AAC49264.1; -.
DR EMBL; AC007661; AAD32767.1; -.
DR EMBL; AY045926; AAK76600.1; -.
DR EMBL; AY079337; AAL85068.1; -.
DR FIR; C84800; C84800.
DR InterPro; IPR001104; Strd5A_dhC.
DR Pfam; PF02544; Steroid_dh; 1.
DR PROSITE; PS50244; S5A_REDUCTASE; 1.
KW Oxidoreductase; Transmembrane.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 51 71 POTENTIAL.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 205 225 POTENTIAL.
FT CONFLICT 198 198 C -> R (IN REF. 1).
SQ SEQUENCE 262 AA; 30635 MW; 88291B8A8AF55664 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 216 WSWA 219

RESULT 34
CY1_RHORU
ID CY1_RHORU STANDARD; PRT; 272 AA.
AC P23135;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c1 precursor.
GN PETC.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-50.
RC STRAIN=FRL;
RX MEDLINE=91094774; PubMed=2176269;
RA Majewski C., Trebst A.;
RT "The pet genes of Rhodospirillum rubrum: cloning and sequencing of
the genes for the cytochrome bcl-complex.";
RL Mol. Gen. Genet. 224:373-382(1990).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis.
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
cytochrome c1 and the Rieske protein.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X55387; CAA39060.1; -.
```


DR PIR; S12258; CCQF1R.
DR InterPro; IPR002326; Cyt C1.
DR InterPro; IPR000345; CytC_heme_BS.
DR Pfam; PF02167; Cytochrome C1; 1.
DR PRINTS; PR00603; CYTOCHROME1.
DR PROSITE; PS00190; CYTOCHROME C; 1.
KW Electron transport; Respiratory chain; Heme; Transmembrane; Signal.
FT SIGNAL 1 24
FT CHAIN 25 272 CYTOCHROME C1.
FT BINDING 61 61 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 64 64 HEME (COVALENT) (BY SIMILARITY).
FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 200 200 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT TRANSMEM 244 261 ANCHORS TO THE MEMBRANE (POTENTIAL).
SQ SEQUENCE 272 AA; 29494 MW; D2575CEBE7CC9332 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
Db 35 DWSW 38

RESULT 35
HRP5_HUMAN STANDARD; PRT; 279 AA.
AC Q96KN8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE H-rev107-like protein 5.
GN HRLP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hughes P.J., Stanway G.;
RT "Identification of a novel member of the H-rev107 protein family.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the H-rev107 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ416558; CAC94942.1; --
DR InterPro; IPR007053; NC.
DR Pfam; PF04970; NC; 1.
SQ SEQUENCE 279 AA; 30281 MW; F6CC44996B0A8E3D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 105 ADWS 108

RESULT 36
CHR2_PSEAE STANDARD; PRT; 280 AA.
ID CHR2_PSEAE
AC Q916V7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotaxis protein methyltransferase 2 (EC 2.1.1.80).
GN CHER2 OR PA0175.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
CC -!- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING
CC CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER
CC RESIDUES IN MCP (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
CC = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
CC -!- SIMILARITY: Contains 1 cher-type methyltransferase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE004455; AAG03565.1; --
DR PIR; H83623; H83623.
DR HSSP; P07801; IAF7.
DR InterPro; IPR000780; Cher_Metransf.
DR InterPro; IPR001601; Methyltransf.
DR Pfam; PF01739; Cher; 1.
DR Pfam; PF03705; Cher N; 1.
DR PRINTS; PR00996; CHERMTFRASE.
DR SMART; SM00138; Metrc; 1.
DR PROSITE; PS0123; CHER; 1.
KW Transferase; Methyltransferase; Complete proteome.
FT DOMAIN 10 280 CHER-TYPE METHYLTRANSFERASE.
SQ SEQUENCE 280 AA; 32028 MW; FD2AF1491DDC57FB CRC64;

Query Match 66.7%; Score 4; DB 1; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 212 ADWS 215

RESULT 37
3MG2_ECOLI STANDARD; PRT; 282 AA.
ID 3MG2_ECOLI
AC P04395;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-3-methyladenine glycosylase II (EC 3.2.2.21) (3-methyladenine-DNA
DE glycosylase II, inducible) (TAG II) (DNA-3-methyladenine glycosidase
DE II).
GN ALKA OR AIDA OR B2068.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;

[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-12 AND 14-20.
MEDLINE=85054800; PubMed=6094528;
Nakabeppu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;
"Structure and expression of the alka gene of Escherichia coli
involved in adaptive response to alkylating agents.";
J. Biol. Chem. 259:13730-13736(1984).
[2]
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
[3]
SEQUENCE FROM N.A.
STRAIN=K12;
MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasubdaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
[4]
CHARACTERIZATION.
MEDLINE=85054799; PubMed=6389535;
Nakabeppu Y., Kondo H., Sekiguchi M.;
"Cloning and characterization of the alka gene of Escherichia coli
that encodes 3-methyladenine DNA glycosylase II.";
J. Biol. Chem. 259:13723-13729(1984).
[5]
SEQUENCE OF 1-2 FROM N.A.
MEDLINE=86313568; PubMed=3529081;
Nakabeppu Y., Sekiguchi M.;
"Regulatory mechanisms for induction of synthesis of repair enzymes
in response to alkylating agents: ada protein acts as a
transcriptional regulator.";
Proc. Natl. Acad. Sci. U.S.A. 83:6297-6301(1986).
[6]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS), AND MUTAGENESIS.
MEDLINE=96319733; PubMed=8706135;
Yamagata Y., Kato M., Odawara K., Tokuno Y., Nakashima Y.,
Matsushima N., Yasumura K., Tomita K.-I., Ihara K., Fujii Y.,
Nakabeppu Y., Sekiguchi M., Fujii S.;
"Three-dimensional structure of a DNA repair enzyme, 3-methyladenine
DNA glycosylase II, from Escherichia coli.";
Cell 86:311-320(1996).
[7]
X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=96319734; PubMed=8706136;
Labahn J., Scharer O.D., Long A., Ezaz-Nikpay K., Verdine G.L.,
Ellenberger T.E.;
"Structural basis for the excision repair of alkylation-damaged DNA.";
Cell 86:321-329(1996).
-!- FUNCTION: HYDROLYSIS OF THE DEOXYRIBOSE N-GLYCOSIDIC BOND TO
EXCISE 3-METHYLADENINE, 3-METHYLGUANINE, 7-METHYLGUANINE,
O2-METHYLTHYMINE, AND O2-METHYLCYTOSINE FROM THE DAMAGED DNA
POLYMER FORMED BY ALKYLATION LESIONS.
-!- CATALYTIC ACTIVITY: Hydrolysis of alkylated DNA, releasing 3-
methyladenine, 3-methylguanine, 7-methylguanine, and 7-
methyladenine.
-!- SUBUNIT: Monomer.
-!- INDUCTION: WHEN E.COLI CELLS ARE EXPOSED TO DOSES OF DNA
ALKYLATING AGENT. IT IS NOT INHIBITED BY REACTION PRODUCTS.
-!- SIMILARITY: Belongs to the alkylbase DNA glycosidase alka family.

CC
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

DR EMBL; K02498; AAA23430.1; -.
DR EMBL; AE000297; AAC75129.1; -.
DR EMBL; D90844; BAA15921.1; -.
DR EMBL; D90845; BAA15926.1; -.
DR EMBL; M13827; -; NOT_ANNOTATED_CDS.
DR PIR; A00904; DGEOMA.
DR PDB; 1MPG; 28-JAN-98.
DR PDB; 1DIZ; 20-JUN-00.
DR EcoGene; EG11222; alka.
DR InterPro; IPR000035; AlbdNA_glycylse.
DR InterPro; IPR003265; Endo_3c.
DR Pfam; PF00730; HhH-GPD; 1.
DR SMART; SM00478; ENDO3C; 1.
DR PROSITE; PS00516; ALKYLBASE_DNA_GLYCOS; 1.
KW DNA repair; Hydrolase; 3D-structure; Complete proteome.
FT SITE 218 218 DETERMINANT FOR SUBSTRATE SPECIFICITY
AND/OR ACTIVITY.
FT ACT SITE 238 238 PROTON ACCEPTOR.
FT MUTAGEN 124 124 Q->A: METHYLMETHANE SULFONATE-RESISTANT.
FT MUTAGEN 218 218 W->A: NO CATALYTIC ACTIVITY,
METHYLMETHANE SULFONATE-SENSITIVE.
FT MUTAGEN 237 237 D->N: MORE THAN 30% CATALYTIC ACTIVITY,
METHYLMETHANE SULFONATE-RESISTANT.
FT MUTAGEN 238 238 D->N: NO CATALYTIC ACTIVITY,
METHYLMETHANE SULFONATE-SENSITIVE.
FT STRAND 2 5
FT HELIX 12 22
FT TURN 25 27
FT STRAND 28 30
FT STRAND 35 41
FT TURN 42 43
FT STRAND 44 53
FT TURN 54 57
FT STRAND 58 63
FT HELIX 65 70
FT HELIX 71 82
FT TURN 83 85
FT HELIX 88 95
FT HELIX 96 99
FT TURN 100 101
FT TURN 103 104
FT HELIX 113 122
FT TURN 123 125
FT HELIX 128 142
FT STRAND 145 145
FT TURN 150 151
FT STRAND 153 153
FT HELIX 158 162
FT TURN 163 163
FT HELIX 166 171
FT TURN 172 173
FT HELIX 176 191
FT TURN 192 192
FT HELIX 202 209
FT TURN 210 211
FT TURN 213 214
FT HELIX 217 227
FT TURN 236 237
FT HELIX 239 244
FT TURN 246 247
FT HELIX 250 257
FT HELIX 258 260
FT TURN 261 262
FT HELIX 264 272
FT TURN 273 273

FT TURN 275 276
SQ SEQUENCE 282 AA; 31393 MW; B66BB5E23019899C CRC64;

Query Match 66.7%; Score 4; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
Db 11 DWSW 14

RESULT 38
RP32_PSEAE STANDARD; PRT; 284 AA.
AC P42378;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA polymerase sigma-32 factor.
GN RPOH OR PA0376.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO;
RX MEDLINE=95245923; PubMed=7728657;
RA Naczynski Z.M., Mueller C., Kropinski A.M.;
RT "Cloning the gene for the heat shock response positive regulator
RT (sigma 32 homolog) from Pseudomonas aeruginosa.";
RL Can. J. Microbiol. 41:75-87(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=95212932; PubMed=7698670;
RA Benvenisti L., Koby S., Rutman A., Giladi H., Yura T.,
RA Oppenheim A.B.;
RT "Cloning and primary sequence of the rpoH gene from Pseudomonas
RT aeruginosa.";
RL Gene 155:73-76(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RA Aramaki H., Fujita M.;
RT "Cloning and sequencing of the gene (rpoH) encoding the heat-shock
RT sigma factor from Pseudomonas aeruginosa.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC THEN IS RELEASED. THIS SIGMA FACTOR IS RESPONSIBLE FOR THE
CC EXPRESSION OF HEAT SHOCK PROMOTERS (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the sigma-70 factor family. Sigma-32
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U09560; AAA92723.1; -.
DR EMBL; S77322; AAB33935.1; -.
DR EMBL; D50052; BAA08769.1; -.
DR EMBL; AE004475; AAG03765.1; -.
DR PIR; JC4040; JC4040.
DR HSSP; P00579; ISIG.
DR InterPro; IPR009043; RNA_pol_sigma.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR007630; Sigma70_r4.
DR InterPro; IPR000943; Sigma70.
DR Pfam; PF04542; sigma70_r2; 1.
DR Pfam; PF04545; sigma70_r4; 1.
DR PRINTS; PR00046; SIGMA70FCT.
DR PROSITE; PS00715; SIGMA70_1; 1.
DR PROSITE; PS00716; SIGMA70_2; 1.
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; Heat shock; Complete proteome.
FT DOMAIN 77 90 POLYMERASE CORE BINDING (POTENTIAL).
FT DNA_BIND 253 272 H-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 284 284 A -> G (IN REF. 1).
SQ SEQUENCE 284 AA; 32581 MW; 282395EE38F21D5D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 216 ADWS 219

RESULT 39
PORI_RHOBL STANDARD; PRT; 289 AA.
AC P39767;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Porin.
GN OPMA.
OS Rhodopseudomonas blastica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1075;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=94191532; PubMed=8142898;
RA Kreusch A., Neubueser A., Schiltz E., Weckesser J., Schulz G.E.;
RT "Structure of the membrane channel porin from Rhodopseudomonas
RT blastica at 2.0-A resolution.";
RL Protein Sci. 3:58-63(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.96 ANGSTROMS).
RX MEDLINE=95055730; PubMed=7525973;
RA Kreusch A., Schulz G.E.;
RT "Refined structure of the porin from Rhodopseudomonas blastica.
RT Comparison with the porin from Rhodobacter capsulatus.";
RL J. Mol. Biol. 243:891-905(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MUTANTS.
RX MEDLINE=98348035; PubMed=9684893;
RA Schmid B., Maveyraud L., Kromer M., Schulz G.E.;
RT "Porin mutants with new channel properties.";
RL Protein Sci. 7:1603-1611(1998).
CC -!- FUNCTION: FORMS CHANNELS THAT ALLOW THE PASSIVE DIFFUSION OF SMALL
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
DR PIR; S38806; S38806.

DR PDB; 1PRN; 24-OCT-94.
DR PDB; 2PRN; 13-JAN-99.
DR PDB; 3PRN; 12-AUG-98.
DR PDB; 5PRN; 12-AUG-98.
DR PDB; 6PRN; 12-AUG-98.
DR PDB; 7PRN; 12-AUG-98.
DR PDB; 8PRN; 12-AUG-98.
DR PDB; 1BH3; 12-AUG-98.
DR PDB; 1H6S; 12-DEC-02.
DR InterPro; IPR001702; Porin_Gram-ve.
DR Pfam; PF00267; Gram-ve_porins; 1.
KW Outer membrane; Transmembrane; Porin; 3D-structure.
FT STRAND 2 15
FT TURN 16 17
FT TURN 20 21
FT STRAND 25 39
FT TURN 42 43
FT STRAND 46 56
FT TURN 57 58
FT HELIX 60 62
FT STRAND 66 66
FT STRAND 70 75
FT TURN 76 77
FT STRAND 78 83
FT HELIX 88 91
FT TURN 95 98
FT STRAND 100 100
FT TURN 101 104
FT STRAND 105 105
FT TURN 107 108
FT TURN 123 124
FT TURN 126 129
FT STRAND 131 138
FT STRAND 142 150
FT TURN 151 154
FT HELIX 157 159
FT STRAND 163 171
FT STRAND 175 183
FT HELIX 185 187
FT TURN 189 190
FT STRAND 193 200
FT STRAND 206 214
FT TURN 216 217
FT TURN 219 220
FT STRAND 223 232
FT TURN 233 234
FT STRAND 235 244
FT TURN 247 248
FT STRAND 252 262
FT TURN 263 264
FT STRAND 265 273
FT TURN 275 276
FT STRAND 279 289
SQ SEQUENCE 289 AA; 30597 MW; 08252D9803A1044C CRC64;

Query Match 66.7%; Score 4; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 168 ADWS 171

RESULT 40
C552_PSEST STANDARD; PRT; 291 AA.
AC P24037;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome c-552 precursor.
GN NIRB.

OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14405 / Zobell;
RX MEDLINE=91160715; PubMed=2001732;
RA Juengst A., Wakabayashi S., Matsubara H., Zumft W.G.;
RT "The nirSTBM region coding for cytochrome cdl-dependent nitrite
RT respiration of Pseudomonas stutzeri consists of a cluster of mono-,
RT di-, and tetraheme proteins.";
RL FEBS Lett. 279:205-209(1991).
RN [2]
RP SEQUENCE OF 24-270.
RC STRAIN=ATCC 14405 / Zobell;
RX MEDLINE=89192360; PubMed=2539041;
RA Denariáz C.M., Liu M.-Y., Payne W.J., le Gall J., Marquez L.,
RA Dunford H.B., van Beeumen J.;
RT "Cytochrome c peroxidase activity of a protease-modified form of
RT cytochrome c-552 from the denitrifying bacterium Pseudomonas
RT perfectomarina.";
RL Arch. Biochem. Biophys. 270:114-125(1989).
CC -!- FUNCTION: May play a role in nitrite reduction. Shows peroxidase
CC activity on proteolytic modification.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- INDUCTION: By anaerobic conditions.
CC -!- PTM: Binds 2 heme groups per molecule.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56813; CAA40152.1; -.
DR PIR; S13938; CCP82S.
DR InterPro; IPR000345; CytC heme BS.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme; Repeat; Periplasmic; Signal.
FT SIGNAL 1 23
FT CHAIN 24 291 CYTOCHROME C-552.
FT BINDING 68 68 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 71 71 HEME 1 (COVALENT) (BY SIMILARITY).
FT METAL 72 72 IRON (HEME 1 AXIAL LIGAND)
FT (BY SIMILARITY).
FT BINDING 157 157 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 161 161 HEME 2 (COVALENT) (BY SIMILARITY).
FT METAL 162 162 IRON (HEME 2 AXIAL LIGAND)
FT (BY SIMILARITY).
FT CONFLICT 59 59 A -> D (IN REF. 2).
FT CONFLICT 229 229 D -> N (IN REF. 2).
FT CONFLICT 268 270 RYH -> SYN (IN REF. 2).
SQ SEQUENCE 291 AA; 30426 MW; DB34BC903CD2687F CRC64;

Query Match 66.7%; Score 4; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 27 ADWS 30

RESULT 41
RSP4_BOVIN
ID RSP4_BOVIN STANDARD; PRT; 295 AA.
AC P26452;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 40S ribosomal protein P40 (C10 protein).

GN LAMR1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Nuchal ligament;

RX MEDLINE=91182754; PubMed=1849001;

RA Grosso L.E., Park P.W., Mecham R.P.;

RT "Characterization of a putative clone for the 67-kilodalton elastin/laminin receptor suggests that it encodes a cytoplasmic protein rather than a cell surface receptor.";

RL Biochemistry 30:3346-3350(1991).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.

CC -!- CAUTION: Was originally thought to be a laminin receptor.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

EMBL; M64923; AAA62713.1; -.

PIR; A38464; A38464.

InterPro; IPR001865; Ribosomal S2.

InterPro; IPR005707; Ribosomal_S2_e/a.

Pfam; PF00318; Ribosomal S2; 1.

PRINTS; PR00395; RIBOSOMALS2.

TIGRFAMs; TIGR01012; Sa S2 E A; 1.

PROSITE; PS00962; RIBOSOMAL_S2_1; 1.

PROSITE; PS00963; RIBOSOMAL_S2_2; 1.

Ribosomal protein; Repeat.

FT REPEAT 247 249 MOTIF A (DWS).

FT REPEAT 266 268 MOTIF A (DWS).

FT REPEAT 275 277 MOTIF A (DWS).

FT REPEAT 264 269 MOTIF B (TEDWSA).

FT REPEAT 273 278 MOTIF B (TEDWSA).

FT REPEAT 285 287 MOTIF C (TEW).

FT REPEAT 292 294 MOTIF C (TEW).

SQ SEQUENCE 295 AA; 32897 MW; 4CAD2FB358BF82C5 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 295;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4

Db 246 ADWS 249

RESULT 42

RSP4_CRIGR STANDARD; PRT; 295 AA.

ID RSP4 CRIGR STANDARD; PRT; 295 AA.

AC P38982;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor).

GN LAMR1.

OS Cricetus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Cricetus.

OX NCBI_TaxID=10029;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RA Chen M.S.M., Laszlo A.A.;

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.

CC -!- CAUTION: Was originally thought to be a laminin receptor.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

EMBL; L16589; AAB46394.1; -.

EMBL; Z22749; CAA80434.1; -.

PIR; S33438; S33438.

InterPro; IPR001865; Ribosomal S2.

InterPro; IPR005707; Ribosomal_S2_e/a.

Pfam; PF00318; Ribosomal S2; 1.

PRINTS; PR00395; RIBOSOMALS2.

TIGRFAMs; TIGR01012; Sa S2 E A; 1.

PROSITE; PS00962; RIBOSOMAL_S2_1; 1.

PROSITE; PS00963; RIBOSOMAL_S2_2; 1.

Ribosomal protein; Repeat.

FT REPEAT 247 249 MOTIF A (DWS).

FT REPEAT 266 268 MOTIF A (DWS).

FT REPEAT 275 277 MOTIF A (DWS).

FT REPEAT 264 269 MOTIF B (TEDWSA).

FT REPEAT 273 278 MOTIF B (TEDWSA).

FT REPEAT 285 287 MOTIF C (TEW).

FT REPEAT 292 294 MOTIF C (TEW).

SQ SEQUENCE 295 AA; 32881 MW; 3E43B4CB01828643 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 295;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4

Db 246 ADWS 249

RESULT 43

RSP4_HUMAN STANDARD; PRT; 295 AA.

ID RSP4 HUMAN STANDARD; PRT; 295 AA.

AC P08865; P11085; P12030; Q16471;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein Mgr1-Ag).

GN LAMR1 OR LAMBR OR RPSA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88320449; PubMed=2970639;

RA Yow H., Wong J.M., Chen H.S., Lee C., Steele G.D. Jr., Chen L.B.;

RT "Increased mRNA expression of a laminin-binding protein in human colon carcinoma: complete sequence of a full-length cDNA encoding the protein.";

RT Proc. Natl. Acad. Sci. U.S.A. 85:6394-6398(1988).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=89282388; PubMed=2543954;

RA van den Ouweland A.M.W., van Duijnhoven H.L.P., Deichmann K.A., van Groningen J.J.M., de Leij L., van de Ven W.J.M.;

RT "Characteristics of a multicopy gene family predominantly consisting of processed pseudogenes.";

RL Nucleic Acids Res. 17:3829-3843(1989).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=96330329; PubMed=8760291;

RA Jackers P., Minoletti F., Belotti D., Clausse N., Sozzi G.,

RA Sobel M.E., Castronovo V.;

RA "Isolation from a multigene family of the active human gene of the

RT metastasis-associated multifunctional protein 37LRP/p40 at chromosome

RT 3p21.3.;"

RL Oncogene 13:495-503(1996).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=92282574; PubMed=1534510;

RA Satoh K., Narumi K., Sakai T., Abe T., Kikuchi T., Matsushima K.,

RA Sindoh S., Motomiya M.;

RA "Cloning of 67-kDa laminin receptor cDNA and gene expression in

RT normal and malignant cell lines of the human lung.;"

RL Cancer Lett. 62:199-203(1992).

RN [5]

RP SEQUENCE FROM N.A.

RA Shi Y., Zhai H., Wang X., Wu H., Ning X., Han Y., Zhang D., Xiao B.,

RA Wu K., Fan D.;

RA "Multidrug resistance associated protein Mgr1-Ag is identical to human

RT 67-KDa laminin receptor precursor.;"

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain, Cervix, Muscle, Placenta, Urinary bladder, and Uterus;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [7]

RP SEQUENCE OF 161-295 FROM N.A.

RX MEDLINE=87016902; PubMed=2429301;

RA Wewer U.M., Liotta L.A., Jaye M., Ricca G.A., Drohan W.N.,

RA Claysmith A.P., Rao C.N., Wirth P., Coligan J.E., Albrechtsen R.,

RA Mudryj M., Sobel M.E.;

RT "Altered levels of laminin receptor mRNA in various human carcinoma

RT cells that have different abilities to bind laminin.;"

RL Proc. Natl. Acad. Sci. U.S.A. 83:7137-7141(1986).

RN [8]

RP SEQUENCE OF 11-295 FROM N.A.

RA Siyanova E.Y., Lukashev V.A., Blinov V.M., Troyanovskii S.M.;

RT "Determination and analysis of the primary sequence of human

RT laminin-binding protein.;"

RL Dokl. Biochem. 313:227-231(1990).

RN [9]

RP SEQUENCE OF 85-209 FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=96163906; PubMed=8586453;

RA Selvamurugan N., Eliceiri G.L.;

RA "The gene for human E2 small nucleolar RNA resides in an intron of a

RT laminin-binding protein gene.;"

RL Genomics 30:400-401(1995).

RN [10]

RP SEQUENCE OF 225-295 FROM N.A.

RX MEDLINE=98248690; PubMed=9582194;

RA Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,

RA Hudson T.J., Tanaka T., Page D.C.;

RT "A map of 75 human ribosomal protein genes.;"

RL Genome Res. 8:509-523(1998).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the S2p family of ribosomal proteins.

CC -!- CAUTION: Was originally thought to be a laminin receptor.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; J03799; AAA36161.1; -

DR EMBL; X15005; CAA33112.1; -

DR EMBL; U43901; AAC50652.1; -

DR EMBL; S37431; AAB22299.1; -

DR EMBL; AF503367; AAM33304.1; -

DR EMBL; BC005391; AAH05391.1; -

DR EMBL; BC008867; AAH08867.1; -

DR EMBL; BC009974; AAH09974.1; -

DR EMBL; BC010054; AAH10054.1; -

DR EMBL; BC010418; AAH10418.1; -

DR EMBL; BC013827; AAH13827.1; -

DR EMBL; BC015654; AAH15654.1; -

DR EMBL; BC034537; AAH34537.1; -

DR EMBL; BC053370; AAH53370.1; -

DR EMBL; M14199; AAA36165.1; -

DR EMBL; X61156; CAA43469.1; -

DR EMBL; U36484; AAC50313.1; -

DR EMBL; AB007146; BAA25812.1; -

DR PIR; A31233; A31233.

DR Genew; HGNC:6502; LAMR1.

DR GK; P08865; -

DR MIM; 150370; -

DR GO; GO:0005055; F:laminin receptor activity; TAS.

DR InterPro; IPR001865; Ribosomal_S2.

DR InterPro; IPR005707; Ribosomal_S2_e/a.

DR Pfam; PF00318; Ribosomal_S2; 1.

DR PRINTS; PR00395; RIBOSOMALS2.

DR TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.

DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.

DR PROSITE; PS00963; RIBOSOMAL_S2_2; 1.

KW Ribosomal protein; Repeat.

FT REPEAT 247 249 MOTIF A (DWS).

FT REPEAT 266 268 MOTIF A (DWS).

FT REPEAT 275 277 MOTIF A (DWS).

FT REPEAT 264 269 MOTIF B (TEDWSA).

FT REPEAT 273 278 MOTIF B (TEDWSA).

FT REPEAT 285 287 MOTIF C (TEW).

FT REPEAT 292 294 MOTIF C (TEW).

FT CONFLICT 60 60 L -> V (IN REF. 8).

FT CONFLICT 84 84 Q -> QVCGTV (IN REF. 2).

FT CONFLICT 211 211 E -> G (IN REF. 4).

FT CONFLICT 228 228 Q -> L (IN REF. 4).

SQ SEQUENCE 295 AA; 32854 MW; C68DDB16B759E79E CRC64;

Query Match 66.7%; Score 4; DB 1; Length 295;

Best Local Similarity 100.0%; Pred.No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4

Db 246 ADWS 249

RESULT 44


```
RSP4_MOUSE
ID_RSP4_MOUSE STANDARD; PRT; 295 AA.
AC P14206;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor).
GN LAMR1 OR P40-8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90057447; PubMed=2531008;
RA Rao C.N., Castronovo V., Schmitt M.C., Wever U.M., Claysmith A.P.,
RA Liotta L.A., Sobel M.E.;
RT "Evidence for a precursor of the high-affinity metastasis-associated
RT murine laminin receptor.";
RL Biochemistry 28:7476-7486(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88189839; PubMed=3357791;
RA Makrides S., Chitpatima S.T., Bandyopadhyay R., Brawerman G.;
RT "Nucleotide sequence for a major messenger RNA for a 40 kilodalton
RT polypeptide that is under translational control in mouse tumor
RT cells.";
RL Nucleic Acids Res. 16:2349-2349(1988).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -!- CAUTION: Was originally thought to be a laminin receptor.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02870; AAA39413.1; -.
DR EMBL; X06406; CAA29696.1; -.
DR SWISS-2DPAGE; P14206; MOUSE.
DR PMMA-2DPAGE; P14206; -.
DR MGD; MGI:105381; Lamr1.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR005707; Ribosomal_S2_e/a.
DR Pfam; PF00318; Ribosomal_S2; 1.
DR PRINTS; PR00395; RIBOSOMALS2.
DR TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
KW Ribosomal protein; Repeat.
FT REPEAT 247 249 MOTIF A (DWS).
FT REPEAT 266 268 MOTIF A (DWS).
FT REPEAT 275 277 MOTIF A (DWS).
FT REPEAT 264 269 MOTIF B (TEDWSA).
FT REPEAT 273 278 MOTIF B (TEDWSA).
FT REPEAT 285 287 MOTIF C (TEW).
FT REPEAT 292 294 MOTIF C (TEW).
FT CONFLICT 18 18 L -> F (IN REF. 2).
FT CONFLICT 155 155 A -> R (IN REF. 2).
SQ SEQUENCE 295 AA; 32719 MW; 449C7E36CF1F1931 CRC64;
```

Query Match 66.7%; Score 4; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
|||
Db 246 ADWS 249

```
RESULT 45
RSP4_RAT
ID_RSP4_RAT STANDARD; PRT; 295 AA.
AC P38983;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor).
GN LAMR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=94164296; PubMed=8119397;
RA Tohgo A., Takasawa S., Munakata H., Yonekura H., Hayaashi N.,
RA Okamoto H.;
RT "Structural determination and characterization of a 40 kDa protein
RT isolated from rat 40 S ribosomal subunit.";
RL FEBS Lett. 340:133-138(1994).
RN [2]
RP SEQUENCE OF 199-295 FROM N.A.
RC STRAIN=Holtzman; TISSUE=Intestinal epithelium;
RX MEDLINE=94357375; PubMed=8076763;
RA Rao M., Manishen W.J., Maheshwari Y., Sykes D.E., Siyanova E.Y.,
RA Tyner A.L., Weiser M.M.;
RT "Laminin receptor expression in rat intestine and liver during
RT development and differentiation.";
RL Gastroenterology 107:764-772(1994).
RN [3]
RP SEQUENCE OF 226-295 FROM N.A.
RA Burns F.R., Rajnavolgy E., Yamashita K., Li X., Shen N.,
RA Heber-Katz E.;
RL Submitted (SEP-1989) to the EMBL/GenBank/DBDJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -!- CAUTION: Was originally thought to be a laminin receptor.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D25224; BAA04953.1; -.
DR EMBL; U04942; AAB60453.1; -.
DR EMBL; M27798; AAA41509.1; -.
DR PIR; S42405; S42405.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR005707; Ribosomal_S2_e/a.
DR Pfam; PF00318; Ribosomal_S2; 1.
DR PRINTS; PR00395; RIBOSOMALS2.
DR TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
KW Ribosomal protein; Repeat.
FT REPEAT 247 249 MOTIF A (DWS).
FT REPEAT 266 268 MOTIF A (DWS).
FT REPEAT 275 277 MOTIF A (DWS).
FT REPEAT 264 269 MOTIF B (TEDWSA).
FT REPEAT 273 278 MOTIF B (TEDWSA).
FT REPEAT 285 287 MOTIF C (TEW).
FT REPEAT 292 294 MOTIF C (TEW).
SQ SEQUENCE 295 AA; 32824 MW; D7DD887DBDD340C CRC64;
```

Query Match 66.7%; Score 4; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98237742; PubMed=9570794;
RA Missler M., Suedhof T.C.;
RT "Neurexophilins form a conserved family of neuropeptide-like
RT glycoproteins.";
RL J. Mol. Neurosci. 18:3630-3638(1998).
CC -!- FUNCTION: May be signaling molecules that resemble neuropeptides
CC and that act by binding to alpha-neurexins and possibly other
CC receptors (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Brain and kidney.
CC -!- PTM: May be proteolytically processed in neuron-like cells (By
CC similarity).
CC -!- SIMILARITY: Belongs to the neurexophilin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF042714; AAD02227.1; -.
KW Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 304 NEUREXOPHILIN 4.
FT DOMAIN 24 84 II.
FT DOMAIN 85 163 III.
FT DOMAIN 164 220 IV (LINKER DOMAIN).
FT DOMAIN 221 304 V (CYS-RICH).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 304 AA; 32945 MW; AD2B30B351DEDB4D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 65 WSWA 68

RESULT 49
CRTE_ERWHE STANDARD; PRT; 307 AA.
ID CRTE_ERWHE STANDARD; PRT; 307 AA.
AC P22873;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29) (GGPP
DE synthetase) (Farnesyltransferase).
GN CRTE.
OS Erwinia herbicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OX NCBI_TaxID=549;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EHO10;
RX MEDLINE=91088634; PubMed=2263648;
RA Armstrong G.A., Alberti M., Hearst J.E.;
RT "Conserved enzymes mediate the early reactions of carotenoid
RT biosynthesis in nonphotosynthetic and photosynthetic prokaryotes.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9975-9979(1990).

RN [2]
RP FUNCTION.
RX MEDLINE=92357711; PubMed=1495965;
RA Math S.K., Hearst J.E., Poulter C.D.;
RT "The crtE gene in Erwinia herbicola encodes geranylgeranyl
RT diphosphate synthase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6761-6764(1992).
CC -!- CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate + isopentenyl
CC diphosphate = diphosphate + geranylgeranyl diphosphate.
CC -!- PATHWAY: Carotenoid biosynthesis.
CC -!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M38424; AAA24819.1; -.
DR EMBL; M87280; AAA64977.1; -.
DR PIR; C39273; C39273.
DR InterPro; IPR000092; Polyprenyl synt.
DR InterPro; IPR008949; Terpenoid synth.
DR Pfam; PF00348; polyprenyl synt; 1.
DR PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
KW Carotenoid biosynthesis; Isoprene biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 33242 MW; 6A534C6194CE9F59 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 298 ADWS 301

RESULT 50
NXP4_HUMAN STANDARD; PRT; 308 AA.
ID NXP4_HUMAN STANDARD; PRT; 308 AA.
AC O95158; Q8N462;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurexophilin 4 precursor.
GN NXP4 OR NPH4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Fayner A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 225-308 FROM N.A.
RX MEDLINE=98237742; PubMed=9570794;
RA Missler M., Suedhof T.C.;
RT "Neurexophilins form a conserved family of neuropeptide-like
RT glycoproteins.";
RL J. Mol. Neurosci. 18:3630-3638(1998).
CC -!- FUNCTION: May be signaling molecules that resemble neuropeptides
CC and that act by binding to alpha-neurexins and possibly other
CC receptors (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in brain, spleen, and testis.
CC -!- PTM: May be proteolytically processed at the boundary between the
CC N-terminal nonconserved and the central conserved domain in
CC neuron-like cells (By similarity).
CC -!- SIMILARITY: Belongs to the neurexophilin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; BC036679; AAH36679.1; -.
DR EMBL; AF043469; AAD02282.1; -.
DR Genew; HGNC:8078; NXPH4.
DR MIM; 604637; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0007218; P:neuropeptide signaling pathway; NAS.
DR KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 308 NEUREXOPHILIN 4.
FT DOMAIN 24 84 II.
FT DOMAIN 85 163 III.
FT DOMAIN 164 224 IV (LINKER DOMAIN).
FT DOMAIN 225 308 V (CYS-RICH).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 226 227 KE -> RG (IN REF. 2).
FT CONFLICT 296 296 Q -> P (IN REF. 2).
SQ SEQUENCE 308 AA; 33110 MW; C34C80A422316F6D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
|
|
|
|
Db 65 WSWA 68

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:24:25 ; Search time 16 Seconds
(without alignments)
36.072 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 6
Sequence: 1 ADWSA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	83.3	374	B83241	conserved hypothet
2	5	83.3	889	E87304	TonB-dependent rec
3	4	66.7	32	A24047	gap junction prote
4	4	66.7	37	A59401	delta-paluit1 - Pa
5	4	66.7	57	AG2302	hypothetical prote
6	4	66.7	88	H95051	hypothetical prote
7	4	66.7	88	D97922	hypothetical prote
8	4	66.7	94	T10250	lectin homolog 2 -
9	4	66.7	95	T36897	probable xylanase
10	4	66.7	97	E53374	type IV prepilin p
11	4	66.7	98	D53374	type IV prepilin p
12	4	66.7	100	H81042	hypothetical prote
13	4	66.7	115	T31781	hypothetical prote
14	4	66.7	118	E90828	probable terminase
15	4	66.7	118	B85686	unknown protein en
16	4	66.7	122	S69909	Ig V-D-J region (M
17	4	66.7	129	E69973	hypothetical prote
18	4	66.7	129	F69902	conserved hypothet
19	4	66.7	132	S65785	mel-13a protein -
20	4	66.7	133	S70967	bfpG protein - Esc
21	4	66.7	133	F84190	hypothetical prote
22	4	66.7	134	AG2926	conserved hypothet
23	4	66.7	134	H98355	hypothetical prote
24	4	66.7	135	B83440	hypothetical prote
25	4	66.7	137	G84174	hypothetical prote
26	4	66.7	139	S54229	Ig mu heavy chain
27	4	66.7	140	A33155	pathogenesis-relat
28	4	66.7	143	T16896	hypothetical prote
29	4	66.7	147	S30974	gene 29 protein -

30	4	66.7	147	2	C72803	gp29 protein - Myc
31	4	66.7	151	2	A81863	hypothetical prote
32	4	66.7	152	2	AI3271	acetyltransferase
33	4	66.7	153	2	B71131	hypothetical prote
34	4	66.7	161	2	A97671	hypothetical prote
35	4	66.7	163	2	T02054	pathogenesis relat
36	4	66.7	166	2	AE0773	conserved hypothet
37	4	66.7	169	1	A35209	cytochrome-c oxida
38	4	66.7	169	1	S12142	cytochrome-c oxida
39	4	66.7	178	2	F82952	ATP synthase delta
40	4	66.7	180	2	H83256	hypothetical prote
41	4	66.7	183	2	G84323	50S ribosomal prot
42	4	66.7	185	2	T28707	hypothetical prote
43	4	66.7	188	2	F95944	hypothetical prote
44	4	66.7	190	2	AC0619	hypothetical bacte
45	4	66.7	191	2	H69387	conserved hypothet
46	4	66.7	194	2	G87453	RNA polymerase sig
47	4	66.7	196	2	G87510	hypothetical prote
48	4	66.7	197	2	E70423	conserved hypothet
49	4	66.7	200	2	G95219	HAM1 protein [impo
50	4	66.7	200	2	T35699	probable sigma fac
51	4	66.7	203	2	D70150	hypothetical prote
52	4	66.7	203	2	E70150	hypothetical prote
53	4	66.7	205	2	G83218	heme acquisition p
54	4	66.7	206	2	C82583	RNA polymerase sig
55	4	66.7	206	2	E83047	hypothetical prote
56	4	66.7	207	2	T03331	gene e36 protein -
57	4	66.7	210	2	A87523	thiol-disulfide in
58	4	66.7	210	2	T26154	hypothetical prote
59	4	66.7	211	2	T03355	gene e12 protein -
60	4	66.7	214	2	G83692	hypothetical prote
61	4	66.7	214	2	AC1057	probable membrane
62	4	66.7	217	2	T17475	enoyl-coA hydratase
63	4	66.7	233	2	G83548	DNA repair protein
64	4	66.7	234	2	T36162	probable integral
65	4	66.7	237	2	AC1316	2-heptaprenyl-1,4-
66	4	66.7	237	2	AC1688	2-heptaprenyl-1,4-
67	4	66.7	239	2	G87550	conserved hypothet
68	4	66.7	240	2	AH3566	hypothetical prote
69	4	66.7	240	2	F82790	GMP synthase XF056
70	4	66.7	241	2	F97752	tolQ protein limpo
71	4	66.7	243	2	E81080	conserved hypothet
72	4	66.7	243	2	AC3600	cellulase (EC 3.2.
73	4	66.7	246	2	T33965	hypothetical prote
74	4	66.7	247	2	E95207	conserved hypothet
75	4	66.7	251	2	E98072	conserved hypothet
76	4	66.7	255	1	UYFVP1	noncapsid protein
77	4	66.7	255	2	D69255	GDP-D-mannose dehy
78	4	66.7	257	2	D87152	conserved hypothet
79	4	66.7	260	2	D83490	probable transcrip
80	4	66.7	261	2	S76510	hypothetical prote
81	4	66.7	262	2	C84800	3-oxo-5-alpha-ster
82	4	66.7	263	2	C87317	hypothetical prote
83	4	66.7	266	2	T35449	hypothetical prote
84	4	66.7	266	2	T15066	hypothetical prote
85	4	66.7	266	2	T29900	hypothetical prote
86	4	66.7	272	1	CCQF1R	ubiquinol-cytochro
87	4	66.7	273	2	B81211	2,3,4,5-tetrahydro
88	4	66.7	273	2	F81787	2,3,4,5-tetrahydro
89	4	66.7	275	2	T05822	hypothetical prote
90	4	66.7	276	2	H86922	probable ABC trans
91	4	66.7	276	2	D82648	hypothetical prote
92	4	66.7	276	2	D82661	hypothetical prote
93	4	66.7	277	2	A97539	MGC1873 protein ho
94	4	66.7	277	2	AD2758	esterase D [import
95	4	66.7	278	2	S75883	hypothetical prote
96	4	66.7	280	2	H83623	probable chemotaxi
97	4	66.7	280	2	C70696	probable transport
98	4	66.7	280	2	AE2031	gamma-tocopherol m
99	4	66.7	282	1	DGECMA	DNA-3-methyladenin
100	4	66.7	282	2	E90988	3-methyl-adenine D
101	4	66.7	282	2	G85833	3-methyl-adenine D
102	4	66.7	284	1	JC4040	transcription init

103 heat-shock sigma f 176 4 66.7 284 2 JC7148
104 transcription regu 177 4 66.7 286 2 D83762
105 DNA-3-methyladenin 178 4 66.7 289 2 A10770
106 porin opma - Rhodo 179 4 66.7 289 2 S38806
107 cytochrome c552 pr 180 4 66.7 291 1 CCPS2S
108 conserved hypothet 181 4 66.7 292 2 D95921
109 conserved hypothet 182 4 66.7 293 2 F87457
110 probable polynucle 183 4 66.7 294 2 D82371
111 ribosomal protein 184 4 66.7 295 1 S42405
112 ribosomal protein 185 4 66.7 295 2 A29395
113 laminin receptor, 186 4 66.7 295 2 S33438
114 33K laminin recept 187 4 66.7 295 2 A38464
115 ribosomal protein 188 4 66.7 295 2 A31233
116 laminin receptor p 189 4 66.7 295 4 JC6530
117 cytochrome-c oxida 190 4 66.7 297 1 S49348
118 hypothetical prote 191 4 66.7 298 2 F87376
119 hypothetical prote 192 4 66.7 299 2 D86199
120 carboxylesterase (193 4 66.7 300 2 I40425
121 carboxylesterase N 194 4 66.7 300 2 C69664
122 ada regulatory pro 195 4 66.7 300 2 G87711
123 haloalkane dehalog 196 4 66.7 302 2 C87395
124 probable transcrip 197 4 66.7 302 2 E83589
125 hypothetical prote 198 4 66.7 303 2 T47356
126 hypothetical prote 199 4 66.7 304 2 T25337
127 hypothetical prote 200 4 66.7 306 2 S19997
128 high-affinity bran 201 4 66.7 307 2 AE3284
129 phytoene synthase 202 4 66.7 308 2 C39273
130 starch synthase DU 203 4 66.7 310 2 T01266
131 L-fucose-specific 204 4 66.7 310 2 JC7853
132 endoglucanase - Th 205 4 66.7 317 2 B72216
133 hypothetical prote 206 4 66.7 317 2 S76618
134 probable methionyl 207 4 66.7 319 2 G71284
135 conserved hypothet 208 4 66.7 319 2 T18245
136 dihydrodipicolinat 209 4 66.7 321 2 AG3131
137 probable dihydrodi 210 4 66.7 321 2 D98156
138 vegetatible incomp 211 4 66.7 324 2 AB3548
139 hypothetical prote 212 4 66.7 325 2 T32282
140 oligopeptide ABC t 213 4 66.7 328 2 E72424
141 nifR3 protein - Az 214 4 66.7 328 2 I39492
142 probable aliphatic 215 4 66.7 330 2 B96027
143 probable cytochrom 216 4 66.7 334 2 T36052
144 hypothetical prote 217 4 66.7 336 2 E98083
145 hypothetical prote 218 4 66.7 337 2 T22570
146 hypothetical prote 219 4 66.7 338 2 S75196
147 conserved hypothet 220 4 66.7 338 2 C75338
148 probable regulator 221 4 66.7 338 2 E91190
149 probable regulator 222 4 66.7 338 2 F86037
150 conserved hypothet 223 4 66.7 339 2 T22571
151 citrate synthase I 224 4 66.7 340 2 H82812
152 conserved hypothet 225 4 66.7 342 2 AD3197
153 conserved hypothet 226 4 66.7 344 2 H70030
154 probable lysosomal 227 4 66.7 344 2 E84526
155 porphobilinogen sy 228 4 66.7 345 2 AG3401
156 phosphate-repressi 229 4 66.7 346 1 BYECPR
157 phosphate-binding 230 4 66.7 346 2 H91211
158 phosphate-binding 231 4 66.7 346 2 H86057
159 periplasmic phosph 232 4 66.7 346 2 AB0956
160 D-amino-acid oxida 233 4 66.7 347 1 S01340
161 D-amino-acid oxida 234 4 66.7 347 1 JX0132
162 ferrochelatase [im 235 4 66.7 347 2 H87715
163 immunogenic protei 236 4 66.7 347 2 D69373
164 gamma-tocopherol m 237 4 66.7 348 2 C96673
165 phosphatidylcholin 238 4 66.7 351 2 S11519
166 protein F25C20.6 I 239 4 66.7 354 2 G86251
167 polyamine transpor 240 4 66.7 354 2 G83194
168 hypothetical prote 241 4 66.7 360 2 T26037
169 Wnt-2 protein - Ca 242 4 66.7 360 2 S32695
170 ferric exochelin b 243 4 66.7 360 2 S60888
171 hypothetical prote 244 4 66.7 361 2 S77525
172 uroporphyrinogen d 245 4 66.7 362 2 S23471
173 pulmonary surfacta 246 4 66.7 363 2 A29072
174 ABC transporter ph 247 4 66.7 364 2 G82595
175 hypothetical prote 248 4 66.7 364 2 S76068

hypothetical prote 365 2 S61636
hydrogenase expres 371 2 A69421
hypothetical prote 372 2 S74532
hypothetical prote 373 2 T34743
hypothetical prote 374 2 G70947
PAS7 protein - yea 375 2 S50228
probable membrane 380 2 AH0781
hypothetical prote 383 2 B83205
hypothetical prote 390 2 A87274
hypothetical prote 390 2 F84196
phosphoglycerate k 394 2 JQ1399
queuine tRNA ribos 394 2 D75256
salicylate 1-monoo 395 2 AI3402
hypothetical prote 399 2 AD1808
bone morphogenetic 400 2 A49147
hypothetical prote 400 2 AF2107
ZK370.5 protein - 401 2 S44666
bone morphogenetic 401 2 JH0689
hypothetical prote 403 2 T33198
hypothetical prote 404 2 D70977
hypothetical prote 405 2 T22675
transcription fact 409 1 A47527
probable replicati 409 2 T47298
protein K04A8.5 [i 411 2 G89074
tetrahydrofolylpol 411 2 E84949
conserved hypothet 411 2 AG3003
hypothetical prote 411 2 B98280
hypothetical prote 415 2 AE1844
hypothetical prote 415 2 G84538
nerve growth facto 416 1 JN0006
hypothetical prote 419 2 D72357
hypothetical prote 421 2 T31787
probable glycerol- 424 2 AI0465
conserved hypothet 429 2 B87039
hypothetical prote 435 2 T36780
hypothetical prote 438 2 D70528
taxadienol acetyl 439 2 T52321
purple acid phosph 441 2 F84560
probable aminoacyl 443 2 T35974
hypothetical prote 445 2 S27492
hypothetical prote 445 2 E82075
hypothetical prote 449 2 H70546
hypothetical prote 450 2 B70506
probable phosphotr 452 2 H91172
probable PTS syste 452 2 AH0964
hypothetical prote 452 2 T33248
exo-alpha-sialidas 453 1 NMIV3
glutamate-cysteine 454 1 NMIV
glutamate-cysteine 457 2 AB2657
probable replicati 457 2 G97438
oxygen-independent 458 2 A84487
hypothetical prote 460 2 A83454
hypothetical prote 462 2 H86018
hypothetical prote 463 2 F81194
hypothetical prote 463 2 E81830
beta-glucosidase h 464 2 AG1146
beta-glucosidase h 464 2 AG1505
hypothetical prote 466 2 S75362
beta-glucosidase B 466 2 F84139
UDP-N-acetylmuramo 467 2 AC3324
hypothetical prote 467 2 H84538
cpsB protein homol 471 2 E56146
GDP-mannose pyroph 471 2 I41251
GDP-manno pyrophos 471 2 I84556
mannose-1-phosphat 471 2 I57096
UDP-N-acetylmuramo 471 2 C87566
centromere/microtu 474 2 T38485
probable transport 476 2 AG1051
hypothetical prote 477 2 S77373
probable nucleotid 477 2 H95936
hypothetical prote 483 2 H90210
hypothetical prote 484 2 A86116
hypothetical 52.9 484 2 D65230

249	4	66.7	484	2	A98275	hypothetical prote
250	4	66.7	487	2	F70765	hypothetical prote
251	4	66.7	489	2	C70655	probable monoxyge
252	4	66.7	491	2	D84967	glucose-6-phosphat
253	4	66.7	491	2	F83383	probable flavin-bi
254	4	66.7	494	2	A86917	probable monoxyge
255	4	66.7	498	2	A87374	hypothetical prote
256	4	66.7	501	2	G72206	GMP synthase - The
257	4	66.7	507	2	AH2717	exopolysphatase
258	4	66.7	507	2	C97499	guanosine-5'-triph
259	4	66.7	516	2	T02189	hypothetical prote
260	4	66.7	527	2	T33175	hypothetical prote
261	4	66.7	527	2	T21830	hypothetical prote
262	4	66.7	532	2	G83424	hypothetical prote
263	4	66.7	534	2	S76219	hypothetical prote
264	4	66.7	536	2	D42463	hypothetical prote
265	4	66.7	537	2	F70597	hypothetical prote
266	4	66.7	542	2	T06728	pectate lyase (EC
267	4	66.7	543	2	JC4812	hyaluronan synthas
268	4	66.7	544	2	S52081	diphosphate-fructo
269	4	66.7	545	2	T27614	hypothetical prote
270	4	66.7	546	2	AB3150	fatty acid CoA lig
271	4	66.7	546	2	G98137	hypothetical prote
272	4	66.7	547	1	A32244	60K cysteine-rich
273	4	66.7	547	2	B43584	60K cysteine-rich
274	4	66.7	547	2	H75632	Na(+)-linked D-ala
275	4	66.7	548	2	B84306	hypothetical prote
276	4	66.7	550	1	VGBE18	glycoprotein E - h
277	4	66.7	553	2	D71515	60K cysteine-rich
278	4	66.7	553	2	T06089	hypothetical prote
279	4	66.7	553	2	AC0065	conserved hypothet
280	4	66.7	554	2	C81671	60 kDa outer membr
281	4	66.7	556	1	S12602	60K cysteine-rich
282	4	66.7	556	2	A86560	60 kDa Cysteine-ri
283	4	66.7	556	2	A69718	squalene-hopene cy
284	4	66.7	557	1	B39439	60K cysteine-rich
285	4	66.7	567	2	AF0308	menaquinone biosyn
286	4	66.7	567	2	T43555	Ras pathway intera
287	4	66.7	567	2	E91095	type III secretion
288	4	66.7	567	2	A85941	type III secretion
289	4	66.7	570	2	AI1828	flavoprotein [impo
290	4	66.7	587	2	AI0180	conserved hypothet
291	4	66.7	599	2	AC3334	metal chelate oute
292	4	66.7	601	1	A64222	heat shock protein
293	4	66.7	602	1	T35760	2',3'-cyclic-nucle
294	4	66.7	602	2	AB2313	hypothetical prote
295	4	66.7	608	2	S09790	hypothetical prote
296	4	66.7	609	2	H90398	hypothetical prote
297	4	66.7	613	2	AH2398	hypothetical prote
298	4	66.7	626	2	T08686	intracellular prot
299	4	66.7	627	2	H86180	hypothetical prote
300	4	66.7	629	2	B95299	probable Cyaf4 ade
301	4	66.7	630	1	G64226	hypothetical prote
302	4	66.7	637	2	T26593	hypothetical prote
303	4	66.7	643	2	E83142	probable transcrip
304	4	66.7	648	2	A48646	amine oxidase (cop
305	4	66.7	654	2	G87517	acetyl/propionyl-C
306	4	66.7	654	2	AG3522	iron-regulated out
307	4	66.7	655	2	AI2556	hypothetical prote
308	4	66.7	657	2	G83906	hypothetical prote
309	4	66.7	665	2	AD0160	probable outer mem
310	4	66.7	665	2	F86181	protein F13M7.17 [
311	4	66.7	678	2	T13773	NADH2 dehydrogenas
312	4	66.7	678	2	A75580	hypothetical prote
313	4	66.7	679	2	AC0333	probable membrane
314	4	66.7	683	2	D82674	TonB-dependent rec
315	4	66.7	689	2	T52060	protein MEDEA [imp
316	4	66.7	692	2	S37976	hypothetical prote
317	4	66.7	698	2	S52674	general sporulatio
318	4	66.7	699	2	AG0371	probable acetyltra
319	4	66.7	700	2	B41897	cellulase (EC 3.2.
320	4	66.7	705	2	A35621	spore germination
321	4	66.7	707	2	S77094	glycogen operon pr

322	4	66.7	714	2	AH2366	hypothetical prote
323	4	66.7	715	2	S70397	zona pellucida gly
324	4	66.7	716	2	S70398	zona pellucida gly
325	4	66.7	720	2	A36942	Fe(II)-pyochelin
326	4	66.7	726	2	D97012	probable processiv
327	4	66.7	730	2	E87251	isoquinoline 1-oxi
328	4	66.7	730	2	S37384	catalase (EC 1.11.
329	4	66.7	730	2	S48813	hypothetical prote
330	4	66.7	731	2	A83410	probable oxidoredu
331	4	66.7	739	2	S15727	cellulase (EC 3.2.
332	4	66.7	745	1	I49101	conserved helix-lo
333	4	66.7	747	2	D70802	hypothetical prote
334	4	66.7	756	2	T49475	related to tol pro
335	4	66.7	757	2	D95103	x-pro dipeptidyl-p
336	4	66.7	758	2	T48815	mixed-linked glucu
337	4	66.7	766	2	T03218	armadillo-like pro
338	4	66.7	766	2	A86198	hypothetical prote
339	4	66.7	768	2	T51209	related to tol pro
340	4	66.7	771	2	A83348	probable aldehyde
341	4	66.7	773	2	JU0135	aldehyde dehydroge
342	4	66.7	783	2	JC6136	kexin-like protein
343	4	66.7	786	2	E87565	conserved hypothet
344	4	66.7	787	2	T49614	related to tol pro
345	4	66.7	795	2	B97971	x-pro dipeptidyl-p
346	4	66.7	802	2	A83125	probable TonB-depe
347	4	66.7	803	2	F90485	hypothetical prote
348	4	66.7	810	2	S44653	F42H10.5 protein -
349	4	66.7	813	2	T04220	H+-transporting AT
350	4	66.7	834	2	S66258	glucosidase I - hu
351	4	66.7	836	2	D87084	phenylalanyl-tRNA
352	4	66.7	836	2	T30312	pinin biosynthetic
353	4	66.7	836	2	D82177	conserved hypothet
354	4	66.7	848	2	E95092	aminopeptidase N [
355	4	66.7	848	2	B97960	membrane alanyl am
356	4	66.7	862	2	H82182	conserved hypothet
357	4	66.7	883	2	C83385	hypothetical prote
358	4	66.7	884	2	S77031	hypothetical prote
359	4	66.7	891	1	RDBHNP	nitrate reductase
360	4	66.7	895	2	A55514	pyruvate dehydroge
361	4	66.7	909	2	AG3419	phage host specifi
362	4	66.7	911	2	T08108	nitrate reductase
363	4	66.7	915	2	A43802	cellulase (EC 3.2.
364	4	66.7	917	2	B81309	isoleucine-tRNA li
365	4	66.7	917	2	T50979	related to tol pro
366	4	66.7	929	2	T38948	hypothetical coile
367	4	66.7	943	2	B83068	probable oxidoredu
368	4	66.7	946	2	F84280	ATP-dependent heli
369	4	66.7	975	2	B34751	hypothetical prote
370	4	66.7	983	2	B45583	receptor tyrosine
371	4	66.7	983	2	A38224	protein-tyrosine k
372	4	66.7	983	2	A45583	receptor tyrosine
373	4	66.7	989	2	T46183	zinc proteinase (E
374	4	66.7	994	2	B82843	valyl-tRNA synthet
375	4	66.7	1011	2	T17430	tol protein - Neur
376	4	66.7	1018	2	T40253	hypothetical prote
377	4	66.7	1019	2	A83613	conserved hypothet
378	4	66.7	1025	2	H86250	hypothetical prote
379	4	66.7	1028	2	T03516	probable outer mem
380	4	66.7	1035	2	T42093	phospholipase D (E
381	4	66.7	1036	2	T13732	phospholipase D (E
382	4	66.7	1036	2	T18530	phospholipase D (E
383	4	66.7	1037	2	T13943	phospholipase D (E
384	4	66.7	1039	2	T28644	Y4JQ protein - Rhi
385	4	66.7	1039	2	S02711	cellulase (EC 3.2.
386	4	66.7	1052	1	A44937	kinetoplast-associ
387	4	66.7	1057	1	OYRTR	atrial natriuretic
388	4	66.7	1057	1	OYMSAR	atrial natriuretic
389	4	66.7	1057	2	I57963	natriuretic peptid
390	4	66.7	1057	2	I55319	guanylyl cyclase A
391	4	66.7	1061	1	OYHUAR	natriuretic peptid
392	4	66.7	1074	2	T17203	phospholipase (EC
393	4	66.7	1074	2	T13725	phospholipase D (E
394	4	66.7	1075	2	T46635	phospholipase D (E

hypothetical prote	322	4	66.7	714	2	AH2366	hypothetical prote
zona pellucida gly	323	4	66.7	715	2	S70397	zona pellucida gly
zona pellucida gly	324	4	66.7	716	2	S70398	zona pellucida gly
Fe(II)-pyochelin	325	4	66.7	720	2	A36942	Fe(II)-pyochelin
probable processiv	326	4	66.7	726	2	D97012	probable processiv
isoquinoline 1-oxi	327	4	66.7	730	2	E87251	isoquinoline 1-oxi
catalase (EC 1.11.	328	4	66.7	730	2	S37384	catalase (EC 1.11.
hypothetical prote	329	4	66.7	730	2	S48813	hypothetical prote
probable oxidoredu	330	4	66.7	731	2	A83410	probable oxidoredu
cellulase (EC 3.2.	331	4	66.7	739	2	S15727	cellulase (EC 3.2.
conserved helix-lo	332	4	66.7	745	1	I49101	conserved helix-lo
hypothetical prote	333	4	66.7	747	2	D70802	hypothetical prote
related to tol pro	334	4	66.7	756	2	T49475	related to tol pro
x-pro dipeptidyl-p	335	4	66.7	757	2	D95103	x-pro dipeptidyl-p
mixed-linked glucu	336	4	66.7	758	2	T48815	mixed-linked glucu
armadillo-like pro	337	4	66.7	766	2	T03218	armadillo-like pro
hypothetical prote	338	4	66.7	766	2	A86198	hypothetical prote
related to tol pro	339	4	66.7	768	2	T51209	related to tol pro
probable aldehyde	340	4	66.7	771	2	A83348	probable aldehyde
aldehyde dehydroge	341	4	66.7	773	2	JU0135	aldehyde dehydroge
kexin-like protein	342	4	66.7	783	2	JC6136	kexin-like protein
conserved hypothet	343	4	66.7	786	2	E87565	conserved hypothet
related to tol pro	344	4	66.7	787	2	T49614	related to tol pro
x-pro dipeptidyl-p	345	4	66.7	795	2	B97971	x-pro dipeptidyl-p
probable TonB-depe	346	4	66.7	802	2	A83125	probable TonB-depe
hypothetical prote	347	4	66.7	803	2	F90485	hypothetical prote
F42H10.5 protein -	348	4	66.7	810	2	S44653	F42H10.5 protein -
H+-transporting AT	349	4	66.7	813	2	T04220	H+-transporting AT
glucosidase I - hu	350	4	66.7	834	2	S66258	glucosidase I - hu
phenylalanyl-tRNA	351	4	66.7	836	2	D87084	phenylalanyl-tRNA
pinin biosynthetic	352	4	66.7	836	2	T30312	pinin biosynthetic
conserved hypothet	353	4	66.7	836	2	D82177	conserved hypothet
aminopeptidase N [354	4	66.7	848	2	E95092	aminopeptidase N [
membrane alanyl am	355	4	66.7	848	2	B97960	membrane alanyl am
conserved hypothet	356	4	66.7	862	2	H82182	conserved hypothet
hypothetical prote	357	4	66.7	883	2	C83385	hypothetical prote
hypothetical prote	358	4	66.7	884	2	S77031	hypothetical prote
nitrate reductase	359	4	66.7	891	1	RDBHNP	nitrate reductase
pyruvate dehydroge	360	4	66.7	895	2	A55514	pyruvate dehydroge
phage host specifi	361	4	66.7	909	2	AG3419	phage host specifi
nitrate reductase	362	4	66.7	911	2	T08108	nitrate reductase
cellulase (EC 3.2.	363	4	66.7	915	2	A43802	cellulase (EC 3.2.
isoleucine-tRNA li	364	4	66.7	917	2	B81309	isoleucine-tRNA li
related to tol pro	365	4	66.7	917	2	T50979	related to tol pro
hypothetical coile	366	4	66.7	917	2	T50979	hypothetical coile
probable oxidoredu	367	4	66.7	917	2	T50979	probable oxidoredu
ATP-dependent heli	368	4	66.7	917	2	T50979	ATP-dependent heli
hypothetical prote	369	4	66.7	917	2	T50979	hypothetical prote
receptor tyrosine	370	4	66.7	917	2	T50979	receptor tyrosine
protein-tyrosine k	371	4	66.7	917	2	T50979	protein-tyrosine k
receptor tyrosine	372	4	66.7	917	2	T50979	receptor tyrosine
zinc proteinase (E	373	4	66.7	917	2	T50979	zinc proteinase (E
valyl-tRNA synthet	374	4	66.7	917	2	T50979	valyl-tRNA synthet
tol protein - Neur	375	4	66.7	917	2	T50979	tol protein - Neur
hypothetical prote	376	4	66.7	917	2	T50979	hypothetical prote
conserved hypothet	377	4	66.7	917	2	T50979	conserved hypothet
hypothetical prote	378	4	66.7	917	2	T50979	hypothetical prote
probable outer mem	379	4	66.7	917	2	T50979	probable outer mem
phospholipase D (E	380	4	66.7	917	2	T50979	phospholipase D (E
phospholipase D (E	381	4	66.7	917	2	T50979	phospholipase D (E
phospholipase D (E	382	4	66.7	917	2	T50979	phospholipase D (E
phospholipase D (E	383	4	66.7	917	2	T50979	phospholipase D (E
Y4JQ protein - Rhi	384	4	66.7	917	2	T50979	Y4JQ protein - Rhi
cellulase (EC 3.2.	385	4	66.7	917	2	T50979	cellulase (EC 3.2.
kinetoplast-associ	386	4	66.7	917	2	T50979	kinetoplast-associ
atrial natriuretic	387	4	66.7	917	2	T50979	atrial natriuretic
atrial natriuretic	388	4	66.7	917	2	T50979	atrial natriuretic
natriuretic peptid	389	4	66.7	917	2	T50979	natriuretic peptid
guanylyl cyclase A	390	4	66.7	917	2	T50979	guanylyl cyclase A
natriuretic peptid	391	4	66.7	917	2	T50979	natriuretic peptid
phospholipase (EC	392	4	66.7	917	2	T50979	phospholipase (EC
phospholipase D (E	393	4	66.7	917	2	T50979	phospholipase D (E
phospholipase D (E	394	4	66.7	917	2	T50979	phospholipase D (E

395	4	66.7	1097	2	S17308	leukemia inhibitor
396	4	66.7	1105	2	A71430	hypothetical prote
397	4	66.7	1107	1	JQ1658	genome polypeptid
398	4	66.7	1125	2	T39052	hypothetical serin
399	4	66.7	1139	2	AI0379	probable potassiu
400	4	66.7	1147	2	D87295	smc protein [impor
401	4	66.7	1215	2	C84848	hypothetical prote
402	4	66.7	1230	2	T07663	soluble starch syn
403	4	66.7	1245	2	E83110	exodeoxyribonuclea
404	4	66.7	1259	2	H65233	ytfN protein - Esc
405	4	66.7	1259	2	G91278	hypothetical prote
406	4	66.7	1259	2	G86119	hypothetical prote
407	4	66.7	1259	2	AE1055	probable exported
408	4	66.7	1266	2	AG2695	conserved hypothet
409	4	66.7	1266	2	G97477	hypothetical prote
410	4	66.7	1271	2	T49009	protein kinase lik
411	4	66.7	1329	2	D87226	conserved hypothet
412	4	66.7	1331	2	A72647	probable surface l
413	4	66.7	1331	2	A48954	mannan endo-1,4-be
414	4	66.7	1334	2	T50568	probable multi-dom
415	4	66.7	1366	2	C85077	probable polypept
416	4	66.7	1423	2	A49206	exo-beta-D-fructos
417	4	66.7	1558	2	AB2457	two-component hybr
418	4	66.7	1573	2	T50113	3-dehydroquinat s
419	4	66.7	1616	1	JQ2144	183K protein - tom
420	4	66.7	1674	2	T01265	starch synthase DU
421	4	66.7	1711	2	T31337	1,4-beta-glucanase
422	4	66.7	1742	2	T17120	cellulase (EC 3.2.
423	4	66.7	1779	2	T31085	xylanase - Caldice
424	4	66.7	1937	2	T03224	probable polyketid
425	4	66.7	1979	1	S03166	myosin heavy chain
426	4	66.7	2472	2	E83594	still frameshift p
427	4	66.7	2559	2	T09144	probable guanine n
428	4	66.7	3005	2	T08841	polypeptid - dour
429	4	66.7	3161	2	T30342	protein HMWp1 - Ye
430	4	66.7	3163	2	T17440	probable polyketid
431	4	66.7	3163	2	AB0233	Yersiniabactin bio
432	4	66.7	3175	1	RRWVEV	genome polypeptid
433	4	66.7	3421	1	WZBEB6	367K tegument prot
434	4	66.7	3534	2	T42567	tegument protein 2
435	4	66.7	3670	2	T36249	CDA peptide synthe
436	4	66.7	4151	2	G70944	probable polyketid
437	3	50.0	7	2	PT0688	T-cell receptor be
438	3	50.0	8	2	PT0724	T-cell receptor be
439	3	50.0	9	2	I58350	gene c-mpl protein
440	3	50.0	10	2	A59272	peptide-N4-(N-acet
441	3	50.0	10	2	B38887	T-cell receptor ga
442	3	50.0	11	2	C38887	T-cell receptor ga
443	3	50.0	11	2	I41946	T-cell receptor ga
444	3	50.0	12	2	H41946	T-cell receptor ga
445	3	50.0	13	2	PH0928	T-cell receptor be
446	3	50.0	14	2	SI4336	mastoparan B - hor
447	3	50.0	15	2	PH0216	agarase (EC 3.2.1.
448	3	50.0	15	2	A48372	benzoyl-CoA ligase
449	3	50.0	15	2	PH1616	Ig H chain V-D-J r
450	3	50.0	16	2	A48630	bothrojaracin - ja
451	3	50.0	17	2	S19614	globin - polychaet
452	3	50.0	20	2	S58382	hypothetical prote
453	3	50.0	20	2	PQ0071	T-cell receptor be
454	3	50.0	21	2	A60420	lens intrinsic mem
455	3	50.0	21	2	S03863	carbonate dehydrat
456	3	50.0	24	2	I38753	ELAV-like neuronal
457	3	50.0	25	2	SI2997	pancreatic endopep
458	3	50.0	25	2	F84066	hypothetical prote
459	3	50.0	30	2	B53088	factor IX/factor X
460	3	50.0	30	2	A53088	hypothetical prote
461	3	50.0	33	2	E82391	cytochrome c6 [imp
462	3	50.0	35	2	AH1838	hypothetical prote
463	3	50.0	36	2	S73127	ycf32 protein - Od
464	3	50.0	36	2	S78239	hypothetical prote
465	3	50.0	36	2	D84275	hypothetical prote
466	3	50.0	36	2	E84416	hypothetical prote
467	3	50.0	37	1	D32038	mu-agatoxin IV - f

468	3	50.0	37	1	E32038	mu-agatoxin V - fu
469	3	50.0	37	1	F32038	mu-agatoxin VI - f
470	3	50.0	37	1	F32038	mu-agatoxin II - f
471	3	50.0	37	2	T11961	hypothetical prote
472	3	50.0	37	2	E97596	hypothetical prote
473	3	50.0	38	1	B35030	curtatoxin II - fu
474	3	50.0	38	1	C32038	mu-agatoxin III -
475	3	50.0	38	1	C35030	curtatoxin III - f
476	3	50.0	39	2	S26937	Ig heavy chain V r
477	3	50.0	39	2	S77904	tax protein - simi
478	3	50.0	40	2	A43853	fructose-bisphosph
479	3	50.0	40	2	B56829	alboaggregin-B alp
480	3	50.0	40	2	A82382	hypothetical prote
481	3	50.0	40	2	C69400	hypothetical prote
482	3	50.0	40	2	A56829	alboaggregin-B bet
483	3	50.0	40	2	S56007	tokaracetin beta c
484	3	50.0	41	2	C97353	probable membrane
485	3	50.0	43	2	C30518	Ig heavy chain V-A
486	3	50.0	43	2	C41397	hypothetical prote
487	3	50.0	43	2	H82619	hypothetical prote
488	3	50.0	44	2	E95248	hypothetical prote
489	3	50.0	45	2	S36709	B7 protein - equin
490	3	50.0	48	2	I79271	tran protein - Esc
491	3	50.0	49	2	PL0163	lysozyme (EC 3.2.1
492	3	50.0	50	2	D90403	hypothetical prote
493	3	50.0	50	2	H90542	hypothetical prote
494	3	50.0	50	2	T00156	hypothetical prote
495	3	50.0	51	2	S00576	hypothetical prote
496	3	50.0	51	2	F82846	hypothetical prote
497	3	50.0	51	2	AB1954	hypothetical prote
498	3	50.0	52	1	RUDV	rubredoxin [valida
499	3	50.0	52	1	JX0241	rubredoxin - Desul
500	3	50.0	52	1	RUME	rubredoxin - Megas
501	3	50.0	52	2	S65620	rubredoxin - Helio
502	3	50.0	52	2	B21440	variant surface gl
503	3	50.0	53	2	S31032	gene 87 protein -
504	3	50.0	53	2	A82960	hypothetical prote
505	3	50.0	53	2	AG2338	hypothetical prote
506	3	50.0	54	2	SI5757	beta-2-microglobul
507	3	50.0	54	2	S22946	SOX-11 protein - A
508	3	50.0	54	2	C72809	gp87 protein - Myc
509	3	50.0	54	2	D82733	hypothetical prote
510	3	50.0	54	2	AE2925	transposase tnp [i
511	3	50.0	55	2	H82976	rubredoxin PA5350
512	3	50.0	55	2	T11171	H+-transporting tw
513	3	50.0	55	2	E90614	ATP synthase F0 ch
514	3	50.0	55	2	E90618	ATP synthase F0 ch
515	3	50.0	55	2	E90620	ATP synthase F0 ch
516	3	50.0	55	2	E90624	ATP synthase F0 ch
517	3	50.0	55	2	E90626	ATP synthase F0 ch
518	3	50.0	55	2	B46485	Ig epsilon chain C
519	3	50.0	55	2	A84180	hypothetical prote
520	3	50.0	55	2	S46977	lysis protein - ph
521	3	50.0	55	2	H95383	protein imported
522	3	50.0	55	2	AD1852	hypothetical prote
523	3	50.0	56	2	B30518	Ig heavy chain V-A
524	3	50.0	56	2	S35645	homeotic protein S
525	3	50.0	56	2	S33894	sox protein - less
526	3	50.0	56	2	S45073	hypothetical prote
527	3	50.0	56	2	C82632	hypothetical prote
528	3	50.0	57	2	H35057	MHC class II histo
529	3	50.0	57	2	T46518	hypothetical prote
530	3	50.0	57	2	T07499	hypothetical prote
531	3	50.0	57	2	A49111	POU homeodomain pr
532	3	50.0	57	2	I58120	gene insl protein
533	3	50.0	58	2	S49347	ccoQ protein - Rho
534	3	50.0	59	1	VIPIA	venom basic protei
535	3	50.0	60	2	D70593	probable rubB prot
536	3	50.0	60	2	T19621	hypothetical prote
537	3	50.0	60	2	C64860	hypothetical prote
538	3	50.0	61	2	E90515	hypothetical prote
539	3	50.0	61	2	A84615	hypothetical prote
540	3	50.0	61	2	AC1443	hypothetical prote

541 3 50.0 61 2 AG2673 hypothetical prote
542 3 50.0 62 2 S53002 mitotic-specific c
543 3 50.0 62 2 D59352 depressant insect-
544 3 50.0 63 2 C42361 DNA-directed RNA p
545 3 50.0 63 2 T12121 NADH dehydrogenase
546 3 50.0 63 2 E89802 hypothetical prote
547 3 50.0 63 2 AI0519 conserved hypothet
548 3 50.0 63 2 AH1856 hypothetical prote
549 3 50.0 64 1 APBPP2 endopeptidase (EC
550 3 50.0 64 2 T16998 S-like ribonucleas
551 3 50.0 64 2 G87525 transcription regu
552 3 50.0 64 2 AC0432 hypothetical prote
553 3 50.0 65 1 RSBPX8 excisionase - phag
554 3 50.0 65 2 A90642 hypothetical prote
555 3 50.0 65 2 S74702 hypothetical prote
556 3 50.0 65 2 A85493 hypothetical prote
557 3 50.0 65 2 E64732 yacG protein - Esc
558 3 50.0 66 2 F95249 conserved domain p
559 3 50.0 66 2 S09855 hypothetical prote
560 3 50.0 66 2 G81965 hypothetical prote
561 3 50.0 66 2 C81872 hypothetical prote
562 3 50.0 66 2 E81150 hypothetical prote
563 3 50.0 66 2 I40095 hypothetical prote
564 3 50.0 66 2 T29847 hypothetical prote
565 3 50.0 66 2 C98114 hypothetical prote
566 3 50.0 67 2 S78325 photosystem II pho
567 3 50.0 67 2 T17586 hypothetical prote
568 3 50.0 67 2 F72226 hypothetical prote
569 3 50.0 67 2 E81975 hypothetical prote
570 3 50.0 68 2 D72428 hypothetical prote
571 3 50.0 68 2 D81806 hypothetical prote
572 3 50.0 68 2 S28483 rfbS protein - Vib
573 3 50.0 68 2 E98055 hypothetical prote
574 3 50.0 69 1 QQECF7 ybeB protein - Esc
575 3 50.0 69 2 C90713 hypothetical prote
576 3 50.0 69 2 G85563 hypothetical prote
577 3 50.0 69 2 C83914 hypothetical prote
578 3 50.0 69 2 AD1147 hypothetical prote
579 3 50.0 69 2 AD1506 hypothetical prote
580 3 50.0 70 2 I30517 Ig heavy chain V-A
581 3 50.0 70 2 A30518 Ig heavy chain V-A
582 3 50.0 70 2 I49450 zinc alpha 2 glyco
583 3 50.0 70 2 AH0182 hypothetical prote
584 3 50.0 71 1 N2NJ1W long neurotoxin 1
585 3 50.0 71 2 A64032 hypothetical prote
586 3 50.0 71 2 E75316 hypothetical prote
587 3 50.0 71 2 B45874 Ig alpha-1 chain C
588 3 50.0 71 2 C45874 Ig alpha-2 chain C
589 3 50.0 72 2 T10937 cellulase (EC 3.2.
590 3 50.0 72 2 JC2384 corazonin precursor
591 3 50.0 72 2 T11887 ATP synthetase sub
592 3 50.0 72 2 F82825 hypothetical prote
593 3 50.0 72 2 AD2464 hypothetical prote
594 3 50.0 73 2 T30357 hypothetical prote
595 3 50.0 73 2 E42524 A-ORF-I protein -
596 3 50.0 73 2 S72715 probable regulator
597 3 50.0 73 2 F70641 hypothetical prote
598 3 50.0 73 2 AE0258 hypothetical phage
599 3 50.0 73 2 AB3264 hypothetical prote
600 3 50.0 74 2 S00166 somatostatin II pr
601 3 50.0 74 2 H84256 hypothetical prote
602 3 50.0 74 2 T32245 hypothetical prote
603 3 50.0 74 2 B82597 hypothetical prote
604 3 50.0 75 2 PQ0805 core protein - hep
605 3 50.0 75 2 S11797 regB protein - Pse
606 3 50.0 76 2 S11704 aminoglycoside 3',
607 3 50.0 76 2 H30517 Ig heavy chain V-A
608 3 50.0 76 2 H64677 hypothetical prote
609 3 50.0 76 2 F71838 probable nadh oxid
610 3 50.0 76 2 T31568 hypothetical prote
611 3 50.0 76 2 AG3626 hypothetical prote
612 3 50.0 77 1 WISMAG alpha-amylase inhi
613 3 50.0 77 2 S35823 envelope protein -

614 3 50.0 77 2 S35844 envelope protein -
615 3 50.0 77 2 S35840 envelope protein -
616 3 50.0 77 2 S35806 envelope protein -
617 3 50.0 77 2 S35841 envelope protein -
618 3 50.0 77 2 S35804 envelope protein -
619 3 50.0 77 2 S35843 envelope prote
620 3 50.0 77 2 C82409 hypothetical prote
621 3 50.0 77 2 T13007 hypothetical prote
622 3 50.0 77 2 T01740 hypothetical prote
623 3 50.0 77 2 AI3031 hypothetical prote
624 3 50.0 77 2 B98254 hypothetical prote
625 3 50.0 78 2 JX0297 alpha-amylase inhi
626 3 50.0 78 2 G30517 Ig heavy chain pre
627 3 50.0 78 2 T32364 hypothetical prote
628 3 50.0 78 2 H82796 hypothetical prote
629 3 50.0 78 2 E82599 hypothetical prote
630 3 50.0 78 2 AG2805 hypothetical prote
631 3 50.0 78 2 AD2028 hypothetical prote
632 3 50.0 79 2 I77326 NADH2 dehydrogenas
633 3 50.0 79 2 I77328 NADH2 dehydrogenas
634 3 50.0 79 2 I77324 NADH2 dehydrogenas
635 3 50.0 79 2 I77322 type III secretion
636 3 50.0 79 2 F91093 hypothetical prote
637 3 50.0 79 2 B82523 hypothetical prote
638 3 50.0 79 2 C95852 hypothetical prote
639 3 50.0 79 2 AI1891 hypothetical prote
640 3 50.0 80 2 T31267 4-oxalocrotonoate
641 3 50.0 80 2 AB1932 hypothetical prote
642 3 50.0 80 2 AE2529 hypothetical prote
643 3 50.0 81 1 IHTF high potential iro
644 3 50.0 81 2 D87361 hypothetical prote
645 3 50.0 81 2 G87197 hypothetical prote
646 3 50.0 81 2 G70534 hypothetical prote
647 3 50.0 81 2 G98177 hypothetical prote
648 3 50.0 81 2 H97567 hypothetical prote
649 3 50.0 81 2 AG2488 hypothetical prote
650 3 50.0 82 2 I36923 gene MHC DQ-beta 1
651 3 50.0 82 2 I50968 MHC class II beta
652 3 50.0 82 2 I50986 MHC class II beta
653 3 50.0 82 2 I51148 MHC class II beta
654 3 50.0 82 2 I61809 gene MHC DQ-beta 1
655 3 50.0 82 2 PQ0804 core protein - hep
656 3 50.0 82 2 T10145 sugar transport pr
657 3 50.0 82 2 T10147 sugar transport pr
658 3 50.0 82 2 T10149 probable hexose tr
659 3 50.0 82 2 T10131 sugar transport pr
660 3 50.0 82 2 T10146 sugar transport pr
661 3 50.0 82 2 T10148 sugar transport pr
662 3 50.0 82 2 T09795 thioesterase homol
663 3 50.0 83 1 S25307 probable allophyc
664 3 50.0 83 2 S57532 hypothetical prote
665 3 50.0 83 2 B72392 hypothetical prote
666 3 50.0 83 2 H85762 probable transposa
667 3 50.0 83 2 AF2563 hypothetical prote
668 3 50.0 84 2 PS0142 replication-associ
669 3 50.0 84 2 F75352 hypothetical prote
670 3 50.0 84 2 D70596 probable whiB1 pro
671 3 50.0 84 2 S12411 hypothetical prote
672 3 50.0 84 2 AC0301 hypothetical prote
673 3 50.0 85 2 T44555 hypothetical prote
674 3 50.0 85 2 T35316 hypothetical prote
675 3 50.0 85 2 B97031 hypothetical prote
676 3 50.0 86 2 F34964 Ig heavy chain V-I
677 3 50.0 86 2 S23992 trbE protein - Esc
678 3 50.0 86 2 S08493 hypothetical prote
679 3 50.0 86 2 T44923 hypothetical prote
680 3 50.0 86 2 AG0108 hypothetical prote
681 3 50.0 86 2 C97474 hypothetical prote
682 3 50.0 87 2 F84161 hypothetical prote
683 3 50.0 87 2 H84234 hypothetical prote
684 3 50.0 87 2 S01071 hypothetical prote
685 3 50.0 87 2 AF2380 hypothetical prote
686 3 50.0 88 1 EDBE51 immediate-early-5

687	3	50.0	88	2	A47760	retrovirus-related	760	3	50.0	97	2	S12416	Ig heavy chain V r
688	3	50.0	88	2	F83979	hypothetical prote	761	3	50.0	97	2	A99427	partial transposas
689	3	50.0	88	2	G97137	hypothetical prote	762	3	50.0	97	2	C56556	fork head homolog
690	3	50.0	88	2	H86125	hypothetical prote	763	3	50.0	97	2	S75011	hypothetical prote
691	3	50.0	89	2	T09494	NADPH-ferrihemopro	764	3	50.0	97	2	S72866	hypothetical prote
692	3	50.0	89	2	E84409	thioredoxin [impor	765	3	50.0	97	2	D64344	hypothetical prote
693	3	50.0	89	2	S61244	probable myristyla	766	3	50.0	97	2	S53474	hypothetical prote
694	3	50.0	89	2	A47099	hypothetical prote	767	3	50.0	97	2	AE2631	hypothetical prote
695	3	50.0	89	2	T08295	hypothetical prote	768	3	50.0	97	2	G97413	hypothetical prote
696	3	50.0	89	2	T46210	hypothetical prote	769	3	50.0	98	1	B53282	beta-2-microglobul
697	3	50.0	89	2	T23831	hypothetical prote	770	3	50.0	98	1	ZNBPF6	gene N protein - p
698	3	50.0	89	2	D82601	hypothetical prote	771	3	50.0	98	2	S26904	Ig heavy chain V r
699	3	50.0	89	2	AC3452	hypothetical prote	772	3	50.0	98	2	S26905	Ig heavy chain V r
700	3	50.0	90	1	MNBPF6	major membrane pro	773	3	50.0	98	2	AG0651	conserved hypothet
701	3	50.0	90	2	A49140	glutathione transf	774	3	50.0	98	2	H64885	ydaS protein - Esc
702	3	50.0	90	2	A65037	hypothetical prote	775	3	50.0	98	2	H91003	probable host-nucl
703	3	50.0	90	2	C85905	hypothetical prote	776	3	50.0	98	2	D72800	gp4 protein - Myco
704	3	50.0	90	2	E91060	hypothetical prote	777	3	50.0	98	2	S30952	gene 4 protein - M
705	3	50.0	90	2	D86690	hypothetical prote	778	3	50.0	98	2	T10114	hypothetical prote
706	3	50.0	90	2	G83334	hypothetical prote	779	3	50.0	98	2	F83404	hypothetical prote
707	3	50.0	90	2	C75345	hypothetical prote	780	3	50.0	98	2	T14691	hypothetical prote
708	3	50.0	90	2	S09252	hypothetical prote	781	3	50.0	98	2	F70769	hypothetical prote
709	3	50.0	91	2	A40076	hypothetical prote	782	3	50.0	98	2	A85638	hypothetical prote
710	3	50.0	91	2	I51179	cytochrome-c oxida	783	3	50.0	98	2	D85848	hypothetical prote
711	3	50.0	91	2	C27578	IGF-I receptor - c	784	3	50.0	98	2	F97804	hypothetical prote
712	3	50.0	91	2	C83414	T-cell receptor be	785	3	50.0	99	1	MGRBB2	beta-2-microglobul
713	3	50.0	91	2	C43940	hypothetical prote	786	3	50.0	99	2	S26803	Ig heavy chain V r
714	3	50.0	91	2	F89879	lactococcin B immu	787	3	50.0	99	2	S26802	Ig heavy chain V r
715	3	50.0	92	2	I84730	conserved hypothet	788	3	50.0	99	2	S26807	Ig heavy chain V r
716	3	50.0	92	2	E90483	beta-2-microglobul	789	3	50.0	99	2	S26899	Ig heavy chain V r
717	3	50.0	92	2	D83065	first ORF in trans	790	3	50.0	99	2	S26801	Ig heavy chain V r
718	3	50.0	92	2	T44734	hypothetical prote	791	3	50.0	99	2	I54312	beta 2-microglobul
719	3	50.0	92	2	C70547	hypothetical prote	792	3	50.0	99	2	T34989	Ig heavy chain V r
720	3	50.0	92	2	T12859	hypothetical prote	793	3	50.0	99	2	S37447	Ig heavy chain V r
721	3	50.0	93	1	A49205	hypothetical prote	794	3	50.0	99	2	S37448	gene E2 protein -
722	3	50.0	93	2	F84175	hypothetical prote	795	3	50.0	99	2	S37441	gene E2 protein -
723	3	50.0	93	2	D70963	hypothetical prote	796	3	50.0	99	2	S37442	gene E2 protein -
724	3	50.0	93	2	AC2676	hypothetical prote	797	3	50.0	99	2	S37444	gene E2 protein -
725	3	50.0	93	2	AE2875	conserved hypothet	798	3	50.0	99	2	E83244	conserved hypothet
726	3	50.0	93	2	B97458	hypothetical prote	799	3	50.0	99	2	F91126	hypothetical prote
727	3	50.0	93	2	AD2047	hypothetical prote	800	3	50.0	99	2	T22965	hypothetical prote
728	3	50.0	94	2	B53374	type IV prepilin p	801	3	50.0	99	2	E85971	hypothetical prote
729	3	50.0	94	2	S10948	sex-determining pr	802	3	50.0	99	2	A65099	conserved hypothet
730	3	50.0	94	2	S75465	hypothetical prote	803	3	50.0	100	2	AE0895	probable phage-rel
731	3	50.0	94	2	D70608	hypothetical prote	804	3	50.0	100	2	AG0447	hypothetical prote
732	3	50.0	94	2	B70930	hypothetical prote	805	3	50.0	100	2	G89963	hypothetical prote
733	3	50.0	94	2	C70662	hypothetical prote	806	3	50.0	100	2	H72680	hypothetical prote
734	3	50.0	94	2	D70560	hypothetical prote	807	3	50.0	100	2	AI0333	probable heme expo
735	3	50.0	94	2	T36982	probable insertion	808	3	50.0	101	2	T10066	probable hexose tr
736	3	50.0	94	2	B82518	hypothetical prote	809	3	50.0	101	2	AI0631	conserved hypothet
737	3	50.0	95	2	I67527	CD33 antigen homol	810	3	50.0	101	2	A71135	probable pheromone
738	3	50.0	95	2	A46422	calcium channel al	811	3	50.0	101	2	D56272	hypothetical prote
739	3	50.0	95	2	E90774	hypothetical prote	812	3	50.0	101	2	T36592	hypothetical prote
740	3	50.0	95	2	G90774	hypothetical prote	813	3	50.0	101	2	G72719	hypothetical prote
741	3	50.0	95	2	E86447	protein F5D14.5 [i	814	3	50.0	101	2	C72659	probable holin pro
742	3	50.0	95	2	C86489	protein T32E20.23	815	3	50.0	101	2	H85688	hypothetical prote
743	3	50.0	95	2	T04973	hypothetical prote	816	3	50.0	101	2	T46506	hypothetical prote
744	3	50.0	95	2	B45519	variant surface gl	817	3	50.0	101	2	G72514	type IV prepilin p
745	3	50.0	95	2	B85637	hypothetical prote	818	3	50.0	102	2	C53374	probable minor tai
746	3	50.0	96	2	E69063	hypothetical prote	819	3	50.0	102	2	F90997	probable minor tai
747	3	50.0	96	2	F69516	hypothetical prote	820	3	50.0	102	2	E85817	probable minor tai
748	3	50.0	97	2	S12958	tachykinin delta p	821	3	50.0	102	2	H64140	ybeB protein homol
749	3	50.0	97	2	S26808	Ig heavy chain V r	822	3	50.0	102	2	S29532	hypothetical prote
750	3	50.0	97	2	FL0118	Ig heavy chain V-I	823	3	50.0	102	2	T13130	protein gp44 - pha
751	3	50.0	97	2	S26805	Ig heavy chain V r	824	3	50.0	102	2	T9387	hypothetical prote
752	3	50.0	97	2	S26804	Ig heavy chain V r	825	3	50.0	102	2	T49387	hypothetical prote
753	3	50.0	97	2	S14474	Ig heavy chain V r	826	3	50.0	102	2	S39687	ywCB protein - Bac
754	3	50.0	97	2	S26806	Ig heavy chain V r	827	3	50.0	102	2	C96595	hypothetical prote
755	3	50.0	97	2	PH0876	Ig heavy chain V-I	828	3	50.0	102	2	T29651	hypothetical prote
756	3	50.0	97	2	G34964	Ig heavy chain V r	829	3	50.0	102	2	S67179	probable membrane
757	3	50.0	97	2	JH0428	Ig gamma chain V r	830	3	50.0	103	1	SXADC2	hexon-associated p
758	3	50.0	97	2	S26898	Ig heavy chain V r	831	3	50.0	103	2	AI1275	thioredoxin homolo
759	3	50.0	97	2	S26906	Ig heavy chain V r	832	3	50.0	103	2	AI1638	thioredoxin homolo

833	3	50.0	103	2	B26167	Ig lambda chain C	906	3	50.0	109	2	E70956	hypothetical prote
834	3	50.0	103	2	C71085	hypothetical prote	907	3	50.0	109	2	G75484	hypothetical prote
835	3	50.0	103	2	AE2121	hypothetical prote	908	3	50.0	109	2	F83457	hypothetical prote
836	3	50.0	103	2	A87435	conserved hypotHet	909	3	50.0	109	2	F88021	protein W10D9.5 [i
837	3	50.0	103	2	JQ0700	hypothetical 11K p	910	3	50.0	109	2	PN0640	polyketide cyclase
838	3	50.0	103	2	S72917	hypothetical prote	911	3	50.0	109	2	C72588	hypothetical prote
839	3	50.0	103	2	D72710	hypothetical prote	912	3	50.0	110	1	RGSAMI	probable regulator
840	3	50.0	103	2	D71047	hypothetical prote	913	3	50.0	110	2	S24250	Ig heavy chain V r
841	3	50.0	104	2	T10287	hypothetical prote	914	3	50.0	110	2	A42573	excinuclease ABC c
842	3	50.0	104	2	S38104	hypothetical prote	915	3	50.0	110	2	S19454	probable membrane
843	3	50.0	104	2	B81045	hypothetical prote	916	3	50.0	110	2	F72487	hypothetical prote
844	3	50.0	104	2	A72598	hypothetical prote	917	3	50.0	110	2	H72567	hypothetical prote
845	3	50.0	104	2	A82395	conserved hypotHet	918	3	50.0	110	2	F91284	hypothetical prote
846	3	50.0	104	2	E87446	hypothetical prote	919	3	50.0	110	2	T12499	hypothetical prote
847	3	50.0	104	2	S17202	protein kinase (EC	920	3	50.0	110	2	T00142	hypothetical prote
848	3	50.0	104	2	F85359	hypothetical prote	921	3	50.0	110	2	AG2575	hypothetical prote
849	3	50.0	104	2	H70823	hypothetical prote	922	3	50.0	111	1	CCEI	cytochrome c - gre
850	3	50.0	104	2	D72744	hypothetical prote	923	3	50.0	111	2	I39601	cytochrome c6 prec
851	3	50.0	104	2	AC0245	conserved hypotHet	924	3	50.0	111	2	AD2337	cytochrome c6 [imp
852	3	50.0	105	1	TXFK	thioredoxin - cory	925	3	50.0	111	2	S08438	vpX protein - huma
853	3	50.0	105	2	H69517	thioredoxin (trx-4	926	3	50.0	111	2	C83320	conserved hypotHet
854	3	50.0	105	2	AG2042	thioredoxin [impor	927	3	50.0	111	2	S56131	12K protein - phag
855	3	50.0	105	2	S44125	Ig lambda chain v	928	3	50.0	111	2	S64145	hypothetical prote
856	3	50.0	105	2	E82047	met repressor VC26	929	3	50.0	111	2	T37114	hypothetical prote
857	3	50.0	105	2	S41856	TyA protein - yeas	930	3	50.0	111	2	T49549	hypothetical prote
858	3	50.0	105	2	F85583	probable tail comp	931	3	50.0	111	2	F82925	hypothetical prote
859	3	50.0	105	2	AE0581	conserved hypotHet	932	3	50.0	111	2	B84058	hypothetical prote
860	3	50.0	105	2	AE1046	SugE protein [impo	933	3	50.0	111	2	I38218	hypothetical prote
861	3	50.0	105	2	S11410	hypothetical prote	934	3	50.0	111	2	F96590	protein-serine/thr
862	3	50.0	105	2	F70587	hypothetical prote	935	3	50.0	111	2	C71227	hypothetical prote
863	3	50.0	105	2	E90831	probable holin pro	936	3	50.0	111	2	AI0687	hypothetical prote
864	3	50.0	105	2	F90335	hypothetical prote	937	3	50.0	112	1	SPRTA	substance P alpha
865	3	50.0	105	2	AH3505	hypothetical prote	938	3	50.0	112	2	T05118	leucoanthocyanidin
866	3	50.0	105	2	C95223	thioredoxin, proba	939	3	50.0	112	2	B47033	AadA2 - Pseudomona
867	3	50.0	105	2	G87591	hypothetical prote	940	3	50.0	112	2	S12155	vpX protein - huma
868	3	50.0	105	2	A83510	hypothetical prote	941	3	50.0	112	2	G70855	hypothetical prote
869	3	50.0	105	2	A82456	probable acetyltra	942	3	50.0	112	2	S75152	hypothetical prote
870	3	50.0	105	2	S52603	hypothetical prote	943	3	50.0	112	2	C70843	probable SdhC subu
871	3	50.0	105	2	E98087	conserved hypotHet	944	3	50.0	112	2	T36564	probable regulator
872	3	50.0	106	2	C69772	thioredoxin homolo	945	3	50.0	112	2	C72605	hypothetical prote
873	3	50.0	106	2	A82870	thioredoxin UU589	946	3	50.0	112	2	H96031	probable transcrip
874	3	50.0	106	2	E84056	thioredoxin' H1 BH3	947	3	50.0	113	2	A34792	Ig heavy chain pre
875	3	50.0	106	2	S37454	Ig mu chain - huma	948	3	50.0	113	2	JL0049	Ig heavy chain V r
876	3	50.0	106	2	H71242	hypothetical prote	949	3	50.0	113	2	D71205	hypothetical prote
877	3	50.0	106	2	T36973	hypothetical prote	950	3	50.0	113	2	T44042	chemokine [importe
878	3	50.0	106	2	C87243	hypothetical prote	951	3	50.0	113	2	G81415	probable periplasm
879	3	50.0	106	2	G97584	hypothetical prote	952	3	50.0	113	2	C75263	hypothetical prote
880	3	50.0	106	2	C83584	conserved hypotHet	953	3	50.0	113	2	A83444	probable lipase PA
881	3	50.0	106	2	A72581	hypothetical prote	954	3	50.0	113	2	AH0397	probable lipoprote
882	3	50.0	107	1	A26622	thioredoxin - Chro	955	3	50.0	114	1	GARB21	Ig heavy chain V-A
883	3	50.0	107	2	G69998	thioredoxin H1 hom	956	3	50.0	114	2	I50553	gonadotropin I bet
884	3	50.0	107	2	AH3504	thioredoxin C-1 [i	957	3	50.0	114	2	B34792	Ig heavy chain pre
885	3	50.0	107	2	B46516	Ig lambda chain v	958	3	50.0	114	2	I72667	cold agglutinin FS
886	3	50.0	107	2	C81172	hypothetical prote	959	3	50.0	114	2	S41365	genome polypotein
887	3	50.0	107	2	B81935	hypothetical prote	960	3	50.0	114	2	S41359	genome polypotein
888	3	50.0	107	2	F64037	hypothetical prote	961	3	50.0	114	2	S41362	genome polypotein
889	3	50.0	107	2	E90976	hypothetical prote	962	3	50.0	114	2	S41366	genome polypotein
890	3	50.0	107	2	C85823	hypothetical prote	963	3	50.0	114	2	S41366	genome polypotein
891	3	50.0	107	2	AF0831	conserved hypotHet	964	3	50.0	114	2	E71034	hypothetical prote
892	3	50.0	108	2	S51759	biphenyl dioxygena	965	3	50.0	114	2	T37926	hypothetical prote
893	3	50.0	108	2	S44190	genome polypotein	966	3	50.0	114	2	D70469	hypothetical prote
894	3	50.0	108	2	AH0679	probable membrane	967	3	50.0	114	2	G69400	conserved hypotHet
895	3	50.0	108	2	AH0176	probable sulfite r	968	3	50.0	114	2	G72510	hypothetical prote
896	3	50.0	108	2	S12193	hypothetical prote	969	3	50.0	114	2	H86625	hypothetical prote
897	3	50.0	108	2	G69261	hypothetical prote	970	3	50.0	114	2	JQ0149	hypothetical 12.6K
898	3	50.0	108	2	F82598	hypothetical prote	971	3	50.0	114	2	G71161	hypothetical prote
899	3	50.0	108	2	G87087	probable membrane	972	3	50.0	115	1	SPRBG	substance P gamma
900	3	50.0	108	2	C95312	hypothetical prote	973	3	50.0	115	2	T07783	leucoanthocyanidin
901	3	50.0	109	1	D42409	biphenyl dioxygena	974	3	50.0	115	2	S47039	tachykinin 1 precu
902	3	50.0	109	1	E41858	biphenyl dioxygena	975	3	50.0	115	2	D34792	Ig heavy chain pre
903	3	50.0	109	1	JC4995	biphenyl dioxygena	976	3	50.0	115	2	C34792	Ig heavy chain pre
904	3	50.0	109	2	D90733	probable minor tai	977	3	50.0	115	2	S41364	genome polypotein
905	3	50.0	109	2	B72615	hypothetical prote	978	3	50.0	115	2	AE3313	protein secretion

979	3	50.0	115	2	T17301	hypothetical prote
980	3	50.0	115	2	H75543	hypothetical prote
981	3	50.0	115	2	F72570	hypothetical prote
982	3	50.0	115	2	G72642	probable surface p
983	3	50.0	115	2	S04677	hypothetical prote
984	3	50.0	115	2	D71194	hypothetical prote
985	3	50.0	116	1	GARB15	Ig heavy chain V-A
986	3	50.0	116	2	F30517	Ig heavy chain pre
987	3	50.0	116	2	S37456	Ig mu chain - huma
988	3	50.0	116	2	B26340	Ig heavy chain pre
989	3	50.0	116	2	S18557	Ig heavy chain V r
990	3	50.0	116	2	A72263	response regulator
991	3	50.0	116	2	G64126	N-acetylmuramoyl-L
992	3	50.0	116	2	A95862	hypothetical prote
993	3	50.0	116	2	D95995	hypothetical prote
994	3	50.0	116	2	AC3319	integrase/recombin
995	3	50.0	116	2	T03472	conserved hypothet
996	3	50.0	116	2	D75355	hypothetical prote
997	3	50.0	116	2	T36999	probable transposa
998	3	50.0	116	2	B69270	hypothetical prote
999	3	50.0	117	1	HVMS8A	Ig heavy chain pre
1000	3	50.0	117	1	HVMS73	Ig heavy chain pre

ALIGNMENTS

RESULT 1
B83241
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83241
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bha
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <STO>
A;Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3230

Query Match	83.3%	Score 5;	DB 2;	Length 374;
Best Local Similarity	100.0%;	Pred. No. 19;		
Matches	5;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	2	DWSWA 6		
Db	81	DWSWA 85		

RESULT 2
E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87304
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-889 <STO>

A;Cross-references: GB:AE005673; NID:gl3421615; PIDN:AAK22433.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0446
Query Match 83.3%; Score 5; DB 2; Length 889;
Best Local Similarity 100.0%;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

Qy	1	ADWSW 5
Db	618	ADWSW 622

RESULT 3
A24047
gap junction protein, cardiac - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Jul-1999
C;Accession: A24047
R;Nicholson, B.J.; Gros, D.B.; Kent, S.B.H.; Hood, L.E.; Revel, J.P.
J. Biol. Chem. 260, 6514-6517, 1985
A;Title: The Mr 28,000 gap junction proteins from rat heart and liver are different but
A;Reference number: A92530; MUID:85207650; PMID:2987225
A;Accession: A24047
A;Molecule type: protein
A;Residues: 1-32 <NIC>
C;Superfamily: gap junction protein
C;Keywords: cardiac muscle; heart; transmembrane protein

Query Match	66.7%;	Score 4;	DB 2;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 44;		
Matches	4;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ADWS 4		
Db	1	ADWS 4		

RESULT 4
A59401
delta-paluit1 - Paracoeelotes luctuosus
C;Species: Paracoeelotes luctuosus
C;Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002
C;Accession: A59401
R;Corzo, G.
Eur. J. Biochem. 267, 5783-5795, 2000
A;Title: Isolation, synthesis and pharmacological characterization of delta-palutoxins I
A;Reference number: A59401
A;Accession: A59401
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-37 <COR>
A;Note: insect-specific sodium channel neurotoxin
C;Superfamily: curtatoxin
F;2-18/Disulfide bonds: #status experimental
F;9-23/Disulfide bonds: #status experimental
F;17-33/Disulfide bonds: #status experimental
F;25-31/Disulfide bonds: #status experimental

A;Accession: A59401				
A;Status: preliminary				
A;Molecule type: protein				
A;Residues: 1-37 <COR>				
A;Note: insect-specific sodium channel neurotoxin				
C;Superfamily: curtatoxin				
F;2-18/Disulfide bonds: #status experimental				
F;9-23/Disulfide bonds: #status experimental				
F;17-33/Disulfide bonds: #status experimental				
F;25-31/Disulfide bonds: #status experimental				
Query Match	66.7%;	Score 4;	DB 2;	Length 37;
Best Local Similarity	100.0%;	Pred. No. 50;		
Matches 4;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

RESULT 5
AG2302
hypothetical protein asl3974 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG2302
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA075673.1; PID:gl17133108; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl3974

Query Match 66.7%; Score 4; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 41 ADWS 44

RESULT 6
H95051
hypothetical protein SP0448 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: H95051
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74609.1; PID:gl14971918; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0448

Query Match 66.7%; Score 4; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 18 ADWS 21

RESULT 7
D97922
hypothetical protein spr0404 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: D97922
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; B
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D97922
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAK99208.1; PID:gl15457967; GSPDB:GN00174
C;Genetics:
A;Gene: spr0404

Query Match 66.7%; Score 4; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 18 ADWS 21

RESULT 8
T10250
lectin homolog 2 - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10250
R;Toyama, T.; Teramoto, H.; Takeba, G.; Tsuji, H.
Plant Cell Physiol. 36, 1349-1359, 1995
A;Title: Cytokinin induces a rapid decrease in the levels of mRNAs for catalase, 3-hydro
A;Reference number: Z16946; MUID:96104306; PMID:8564304
A;Accession: T10250
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-94 <TOY>
A;Cross-references: EMBL:D63388; NID:gl1199482; PIDN:BAA09704.1; PID:gl1199483
A;Experimental source: seedling; cotyledon

Query Match 66.7%; Score 4; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 35 WSWA 38

RESULT 9
T36897
probable xylanase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002
C;Accession: T36897
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
A;Accession: T36897
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-95 <SEE>
A;Cross-references: EMBL:AL096743; PIDN:CAB46384.1; GSPDB:GN00070; SCOEDB:SCI7.01c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCI7.01c
C;Superfamily: Xylan 1,4-beta-xylosidase (EC 3.2.1.37)

Query Match 66.7%; Score 4; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 18 ADWS 21

RESULT 10
E53374
type IV prepilin peptidase (EC 3.4.99.-) pILD - Neisseria subflava (strain LNP3260) (frag
N;Contains: type IV pilin N-methyltransferase (EC 2.1.1.-)
C;Species: Neisseria subflava
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 29-Jan-1999

C;Accession: E53374
R;Dupuy, B.; Pugsley, A.P.
J. Bacteriol. 176, 1323-1331, 1994
A;Title: Type IV prepilin peptidase gene of *Neisseria gonorrhoeae* MS11: presence of a re
A;Reference number: A53374; MUID:94156836; PMID:7906688
A;Accession: E53374
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-97 <DUP>
C;Genetics:
A;Gene: piliD
C;Superfamily: type IV prepilin peptidase
C;Keywords: hydrolase; methyltransferase; S-adenosylmethionine

Query Match 66.7%; Score 4; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 19 WSWA 22

RESULT 11
D53374
type IV prepilin peptidase (EC 3.4.99.-) - *Neisseria sicca* (strain LNP3265) (fragment)
N;Contains: type IV pilin N-methyltransferase (EC 2.1.1.-)
C;Species: *Neisseria sicca*
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 29-Jan-1999
C;Accession: D53374
R;Dupuy, B.; Pugsley, A.P.
J. Bacteriol. 176, 1323-1331, 1994
A;Title: Type IV prepilin peptidase gene of *Neisseria gonorrhoeae* MS11: presence of a re
A;Reference number: A53374; MUID:94156836; PMID:7906688
A;Accession: D53374
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-98 <DUP>
C;Superfamily: type IV prepilin peptidase
C;Keywords: hydrolase; methyltransferase; S-adenosylmethionine

Query Match 66.7%; Score 4; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 20 WSWA 23

RESULT 12
H81042
hypothetical protein NMB1782 [imported] - *Neisseria meningitidis* (strain MC58 serogroup
C;Species: *Neisseria meningitidis*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: H81042; G81988
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <TET>
A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42122.1; PID:g722703
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83970.1; PID:g7379410
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB1782; NMA0683; NMA0684
C;Superfamily: *Neisseria meningitidis* hypothetical protein NMB1782

Query Match 66.7%; Score 4; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
Db 77 DWSW 80

RESULT 13
T31781
hypothetical protein F13H6.2 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T31781
R;Jones, K.; Wohldmann, P.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of *C. elegans* cosmid F13H6.
A;Reference number: Z21085
A;Accession: T31781
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-115 <JON>
A;Cross-references: EMBL:AF016437; PIDN:AAB65884.1; GSPDB:GN00023; CESP:F13H6.2
A;Experimental source: strain Bristol N2; clone F13H6
C;Genetics:
A;Gene: CESP:F13H6.2
A;Map position: 5
A;Introns: 52/1; 92/3
C;Superfamily: *Caenorhabditis elegans* hypothetical protein F13H6.2

Query Match 66.7%; Score 4; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 95 ADWS 98

RESULT 14
E90828
probable terminase small subunit [imported] - *Escherichia coli* (strain O157:H7, substrain
C;Species: *Escherichia coli*
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: E90828
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genor
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90828
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA035020.1; PID:g13361061; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1597

Query Match 66.7%; Score 4; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ADWS 4
Db	35 ADWS 38
RESULT 15	
B85686	
unknown protein encoded by prophage CP-933C [imported] - Escherichia coli (strain O157:H7)	
C;Species: Escherichia coli	
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001	
C;Accession: B85686	
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew	
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,	
Nature 409, 529-533, 2001	
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.	
A;Reference number: A85480; MUID:21074935; PMID:11206551	
A;Accession: B85686	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-118 <STO>	
A;Cross-references: GB:AE005174; NID:g12514775; PIDN:AAG55950.1; GSPDB:GN00145; UWGP:Z18	
A;Experimental source: strain O157:H7, substrain EDL933	
C;Genetics:	
A;Gene: Z1853	
Query Match 66.7%; Score 4; DB 2; Length 118;	
Best Local Similarity 100.0%; Pred. No. 1.3e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ADWS 4
Db	35 ADWS 38
RESULT 16	
S69909	
Ig V-D-J region (MS) - human	
C;Species: Homo sapiens (man)	
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000	
C;Accession: S69909	
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.	
Leukemia 8, 1285-1289, 1994	
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi	
A;Reference number: S69909; MUID:94335315; PMID:8057663	
A;Accession: S69909	
A;Status: preliminary; nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-122 <SAH>	
A;Cross-references: EMBL:Z33399; NID:g871348; PIDN:CAA83850.1; PID:g871349	
A;Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are	
C;Superfamily: immunoglobulin v region; immunoglobulin homology	
F;15-97/Domain: immunoglobulin homology <IMM>	
Query Match 66.7%; Score 4; DB 2; Length 122;	
Best Local Similarity 100.0%; Pred. No. 1.4e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2 DWSW 5
Db	33 DWSW 36
RESULT 17	
E69973	
hypothetical protein yrdN - Bacillus subtilis	
C;Species: Bacillus subtilis	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000	
C;Accession: E69973	
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter	
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd	
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.	

Nature 390, 249-256, 1997	
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc	
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.,	
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,	
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,	
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,	
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,	
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,	
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,	
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K	
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.	
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.	
A;Reference number: A69580; MUID:98044033; PMID:9384377	
A;Accession: E69973	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA	
A;Residues: 1-129 <KUN>	
A;Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14607.1; PID:g2635111	
A;Experimental source: strain 168	
C;Genetics:	
A;Gene: yrdN	
C;Superfamily: hypothetical protein yrdN	
Query Match 66.7%; Score 4; DB 1; Length 129;	
Best Local Similarity 100.0%; Pred. No. 1.4e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ADWS 4
Db	113 ADWS 116
RESULT 18	
F69902	
conserved hypothetical protein yodA - Bacillus subtilis	
C;Species: Bacillus subtilis	
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000	
C;Accession: F69902	
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter	
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho	
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.	
Nature 390, 249-256, 1997	
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc	
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.,	
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,	
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,	
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,	
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,	
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,	
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,	
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K	
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.	
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.	
A;Reference number: A69580; MUID:98044033; PMID:9384377	
A;Accession: F69902	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA	
A;Residues: 1-129 <KUN>	
A;Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13844.1; PID:g2634345	
A;Experimental source: strain 168	
C;Genetics:	
A;Gene: yodA	
C;Superfamily: hypothetical protein yrdN	
Query Match 66.7%; Score 4; DB 2; Length 129;	
Best Local Similarity 100.0%; Pred. No. 1.4e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ADWS 4
Db	113 ADWS 116

RESULT 19
S65785
mel-13a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S65785
R;Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene
A;Reference number: S65785; MUID:96180310; PMID:8597592
A;Accession: S65785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <TET>
A;Cross-references: EMBL:U35309
C;Genetics:
A;Gene: mel-13
C;Superfamily: mouse mel-13a protein
C;Keywords: alternative splicing
Query Match 66.7%; Score 4; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSW 5
Db 58 DWSW 61
RESULT 20
S70967
bfpG protein - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Jun-2000
C;Accession: S70967
R;Stone, K.D.; Zhang, H.Z.; Carlson, L.K.; Donnenberg, M.S.
Mol. Microbiol. 20, 325-337, 1996
A;Title: A cluster of fourteen genes from enteropathogenic Escherichia coli is sufficient
A;Reference number: S70966; MUID:96310370; PMID:8733231
A;Accession: S70967
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-133 <STO>
A;Cross-references: EMBL:Z68186; NID:g1122399; PIDN:CAA92327.1; PID:g1122401
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C;Genetics:
A;Gene: bfpG
A;Start codon: GTG
C;Superfamily: Escherichia coli bfpG protein
Query Match 66.7%; Score 4; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
Db 50 ADWS 53
RESULT 21
F84190
hypothetical protein Vng0311h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84190
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84190

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <STO>
A;Cross-references: GB:AE004437; NID:g10579938; PIDN:AAG18890.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG0311H
Query Match 66.7%; Score 4; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
Db 78 ADWS 81
RESULT 22
AG2926
conserved hypothetical protein Atu3013 [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AG2926
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutnyavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG2926
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL43829.1; PID:g17741370; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3013
A;Map position: linear chromosome
Query Match 66.7%; Score 4; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
Db 20 ADWS 23
RESULT 23
H98355
hypothetical protein AGR_L_3577 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: H98355
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H98355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK90370.1; PID:g15160412; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_3577
A;Map position: linear chromosome
Query Match 66.7%; Score 4; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 20 ADWS 23

RESULT 24
B83440
hypothetical protein PA1645 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83440
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83440
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-135 <STO>
A;Cross-references: GB:AE004592; GB:AE004091; NID:g9947609; PIDN:AAG05034.1; GSPDB:GN00138
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1645

Query Match 66.7%; Score 4; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 19 ADWS 22

RESULT 25
G84174
hypothetical protein Vng0143h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84174
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonka, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lin, J.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <STO>
A;Cross-references: GB:AE004437; NID:g10579791; PIDN:AAG18763.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG0143H

Query Match 66.7%; Score 4; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 92 ADWS 95

RESULT 26
S54229
Ig mu heavy chain V region precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C;Accession: S54229
R;Dufour, V.; Nau, F.
submitted to the EMBL Data Library, April 1995

A;Description: Sheep immunoglobulin mu heavy chain variable region sequence.
A;Reference number: S54225
A;Accession: S54229
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <DUF>
A;Cross-references: EMBL:Z49163; NID:g794097; PIDN:CAA89032.1; PID:g794098
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 4; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 118 WSWA 121

RESULT 27
A33155
pathogenesis-related protein 1 - maize
C;Species: Zea mays (maize)
C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 31-Dec-1993
C;Accession: A33155
R;Gillikin, J.; Burkhardt, W.; Graham, J.S.
submitted to the Protein Sequence Database, February 1991
A;Reference number: A33155
A;Accession: A33155
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-140 <GIL>
C;Superfamily: pathogenesis-related leaf protein

Query Match 66.7%; Score 4; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 64 ADWS 67

RESULT 28
T16896
hypothetical protein T19D7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16896
R;Minx, P.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid T19D7.
A;Reference number: Z18600
A;Accession: T16896
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-143 <MIN>
A;Cross-references: EMBL:U56961; NID:g1293805; PID:g1293807; PIDN:AAA98712.1; GSPDB:GN00138
A;Experimental source: strain Bristol N2; clone T19D7
C;Genetics:
A;Gene: CESP:T19D7.2
A;Map position: X
A;Introns: 28/3; 52/1; 113/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T19D7.2

Query Match 66.7%; Score 4; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 120 ADWS 123

RESULT 29
S30974
gene 29 protein - Mycobacterium phage L5
C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C;Accession: S30974
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic transduction
A;Reference number: S30949; MUID:93211283; PMID:8459767
A;Accession: S30974
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-147 <DON>
A;Cross-references: EMBL:Z18946; NID:g15859; PIDN:CAA79405.1; PID:g15885
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C;Genetics:
A;Gene: 29
C;Superfamily: Mycobacterium phage L5 gene 29 protein

Query Match 66.7%; Score 4; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 40 ADWS 43

RESULT 30
C72803
gp29 protein - Mycobacterium phage D29
C;Species: Mycobacterium phage D29
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 20-Apr-2001
C;Accession: C72803
R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 279, 143-164, 1998
A;Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.
A;Reference number: A72800; MUID:98300335; PMID:9636706
A;Accession: C72803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <FOR>
A;Cross-references: GB:AF022214; NID:g3172250; PIDN:AAC18470.1; PID:g3172277
C;Genetics:
A;Gene: 29
C;Superfamily: Mycobacterium phage L5 gene 29 protein

Query Match 66.7%; Score 4; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 40 ADWS 43

RESULT 31
A81863
hypothetical protein NMA1678 [imported] - Neisseria meningitidis (strain Z2491 serogroup B)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81863
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81863
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-151 <PAR>
A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84906.1; PID:g738031;
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1678

Query Match 66.7%; Score 4; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 39 ADWS 42

RESULT 32
AI3271
acetyltransferase (EC 2.3.1.-) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3271
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis;
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51340.1; PID:g17982038; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0158
A;Map position: 1
C;Keywords: acyltransferase

Query Match 66.7%; Score 4; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 141 ADWS 144

RESULT 33
B71131
hypothetical protein PH0815 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71131
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: B71131
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-153 <KAW>
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29908.1; PID:g3257225
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0815
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0815

Query Match 66.7%; Score 4; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5

Db 125 DWSW 128
|||||
RESULT 34
A97671
hypothetical protein AGR_C_4708 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: A97671
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97671
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88322.1; PID:g15157798; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_4708
A;Map position: circular chromosome
Query Match 66.7%; Score 4; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
|||||
Db 34 ADWS 37
RESULT 35
T02054
pathogenesis related protein-1 - maize
C;Species: Zea mays (maize)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 11-May-2000
C;Accession: T02054
R;Morris, S.W.; Vernooij, B.; Titatarn, S.; Starrett, M.; Thomas, S.; Wiltse, C.C.; Fred
Mol. Plant Microbe Interact. 11, 643-658, 1998
A;Title: Induced resistance responses in maize.
A;Reference number: Z14524; MUID:98313983; PMID:9650297
A;Accession: T02054
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-163 <MOR>
A;Cross-references: EMBL:U82200; NID:g3290003; PIDN:AAC25629.1; PID:g3290004
C;Genetics:
A;Gene: PR-1
C;Superfamily: pathogenesis-related leaf protein
Query Match 66.7%; Score 4; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
|||||
Db 87 ADWS 90
RESULT 36
AE0773
conserved hypothetical protein STY2358 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0773
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0773
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02507.1; PID:g16503371; GSPDB:GN00176
C;Genetics:
A;Gene: STY2358
Query Match 66.7%; Score 4; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 WSWA 6
|||||
Db 133 WSWA 136
RESULT 37
A35209
cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 11-Jun-1999
C;Accession: A35209; S12724; S04070; S04593; S14190; S65373
R;Yamada, M.; Amuro, N.; Goto, Y.; Okazaki, T.
J. Biol. Chem. 265, 7687-7692, 1990
A;Title: Structural organization of the rat cytochrome c oxidase subunit IV gene.
A;Reference number: A35209; MUID:90237079; PMID:2159010
A;Accession: A35209
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <YAM>
A;Cross-references: GB:J05425; NID:g203516; PIDN:AAA40949.1; PID:g203517
R;Amuro, N.; Yamada, M.; Goto, Y.; Okazaki, T.
Nucleic Acids Res. 18, 3992, 1990
A;Title: Complete nucleotide sequence of the gene encoding rat cytochrome c oxidase subunit
A;Reference number: S12724; MUID:90326528; PMID:2165254
A;Accession: S12724
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <AMU>
A;Cross-references: EMBL:J05425; NID:g203516; PIDN:AAA40949.1; PID:g203517
R;Goto, Y.; Amuro, N.; Okazaki, T.
Nucleic Acids Res. 17, 2851, 1989
A;Title: Nucleotide sequence of cDNA for rat brain and liver cytochrome c oxidase subunit
A;Reference number: S04070; MUID:89240039; PMID:2541414
A;Accession: S04070
A;Molecule type: mRNA
A;Residues: 1-169 <GOT>
A;Cross-references: EMBL:X14209; NID:g55989; PIDN:CAA32426.1; PID:g55990
R;Gopalan, G.; Droste, M.; Kadenbach, B.
Nucleic Acids Res. 17, 4376, 1989
A;Title: Nucleotide sequence of cDNA encoding subunit IV of cytochrome c oxidase from fet
A;Reference number: S04593; MUID:89296488; PMID:2544859
A;Accession: S04593
A;Molecule type: mRNA
A;Residues: 1-169 <GOP>
A;Cross-references: EMBL:X15029; NID:g55980; PIDN:CAA33133.1; PID:g55981
R;Virbasius, J.V.; Scarpulla, R.C.
Nucleic Acids Res. 18, 6581-6586, 1990
A;Title: The rat cytochrome c oxidase subunit IV gene family: tissue-specific and hormone
A;Reference number: S14190; MUID:91067442; PMID:2174541
A;Accession: S14190
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-169 <VIR>
A;Cross-references: EMBL:X54081; NID:g57030; PIDN:CAA38018.1; PID:g57031
A;Experimental source: strain Sprague Dawley
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-termi

C;Genetics:
A;Gene: rp118p
C;Superfamily: rat ribosomal protein L5

Query Match 66.7%; Score 4; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 138 ADWS 141

RESULT 42
T28707
hypothetical protein T21D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 06-Oct-2000
C;Accession: T28707
R;Woessner, J.
Submitted to the EMBL Data Library, August 1997
A;Description: The sequence of C. elegans cosmid T21D12.
A;Reference number: Z20514
A;Accession: T28707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-185 <WOE>
A;Cross-references: EMBL:AF016687; PIDN:AAC48089.1; GSPDB:GN00022; CESP:T21D12.1
A;Experimental source: strain Bristol N2; clone T21D12
C;Genetics:
A;Gene: CESP:T21D12.1
A;Map position: 4
A;Introns: 17/1; 51/1; 127/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M02B7.2

Query Match 66.7%; Score 4; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 95 ADWS 98

RESULT 43
F95944
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F95944
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95944
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49222.1; PID:g15140708; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyma, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB21156
A;Genome: plasmid

Query Match 66.7%; Score 4; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 59 ADWS 62

RESULT 44
AC0619
hypothetical bacteriophage protein STY1027 [imported] - Salmonella enterica subsp. enter
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0619
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05421.1; PID:g16502182; GSPDB:GN00176
C;Genetics:
A;Gene: STY1027

Query Match 66.7%; Score 4; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 55 ADWS 58

RESULT 45
H69387
conserved hypothetical protein AF1105 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: H69387
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glock, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <KLE>
A;Cross-references: GB:AE001027; GB:AE000782; NID:g2689350; PIDN:AAB90133.1; PID:g2649475

Query Match 66.7%; Score 4; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 98 ADWS 101

RESULT 46
G87453
RNA polymerase sigma-70 factor, ECF subfamily [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: G87453
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87453
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <STO>
A;Cross-references: GB:AE005673; NID:gl3423053; PIDN:AAK23627.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1649

Query Match 66.7%; Score 4; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 148 ADWS 151

RESULT 47
G87510
hypothetical protein CC2112 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: G87510
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <STO>
A;Cross-references: GB:AE005673; NID:gl3423599; PIDN:AAK24083.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2112

Query Match 66.7%; Score 4; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 160 WSWA 163

RESULT 48
E70423
conserved hypothetical protein aq_1421 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: E70423
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: E70423
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-197 <AQF>
A;Cross-references: GB:AE000739; NID:g2983813; PIDN:AAC07381.1; PID:g2983825; GB:AE00069
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1421

Query Match 66.7%; Score 4; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 51 WSWA 54

RESULT 49
G95219
HAM1 protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: G95219
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95219
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75952.1; PID:gl4973383; GSPDB:GN00164; TIGR:SP49
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1880
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0226

Query Match 66.7%; Score 4; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 135 ADWS 138

RESULT 50
T35699
probable sigma factor - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: T35699
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21548
A;Accession: T35699
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-200 <MUR>
A;Cross-references: EMBL:AL021411; PIDN:CAA16191.1; GSPDB:GN00070; SCOEDB:SC7H1.04
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC7H1.04
C;Superfamily: transcription initiation factor sigma E

Query Match 66.7%; Score 4; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 38 ADWS 41

Search completed: July 23, 2004, 13:27:53
Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:27:25 ; Search time 42 seconds
(without alignments)
44.736 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 6
Sequence: 1 ADWSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1288442 seqs, 313154207 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	10	US-09-847-946A-41
2	6	100.0	6	10	US-09-847-946A-73
3	6	100.0	7	10	US-09-847-946A-77
4	6	100.0	8	10	US-09-847-946A-70
5	6	100.0	8	10	US-09-847-946A-78
6	6	100.0	9	10	US-09-847-946A-69
7	6	100.0	9	10	US-09-847-946A-72
8	6	100.0	9	10	US-09-847-946A-75
9	6	100.0	9	10	US-09-847-946A-76
10	6	100.0	10	10	US-09-847-946A-71
11	6	100.0	10	10	US-09-847-946A-74
12	6	100.0	11	10	US-09-847-946A-68
13	5	83.3	6	9	US-09-847-940B-4
14	5	83.3	6	9	US-09-847-940B-5
15	5	83.3	6	10	US-09-847-946A-4

16	5	83.3	6	10	US-09-847-946A-5	Sequence 5, Appli
17	5	83.3	6	10	US-09-847-946A-39	Sequence 39, Appl
18	5	83.3	6	10	US-09-847-946A-40	Sequence 40, Appl
19	5	83.3	6	10	US-09-847-946A-51	Sequence 51, Appl
20	5	83.3	6	10	US-09-847-946A-62	Sequence 62, Appl
21	5	83.3	7	10	US-09-847-946A-55	Sequence 55, Appl
22	5	83.3	7	10	US-09-847-946A-66	Sequence 66, Appl
23	5	83.3	8	10	US-09-847-946A-48	Sequence 48, Appl
24	5	83.3	8	10	US-09-847-946A-56	Sequence 56, Appl
25	5	83.3	8	10	US-09-847-946A-59	Sequence 59, Appl
26	5	83.3	8	10	US-09-847-946A-67	Sequence 67, Appl
27	5	83.3	9	10	US-09-847-946A-47	Sequence 47, Appl
28	5	83.3	9	10	US-09-847-946A-50	Sequence 50, Appl
29	5	83.3	9	10	US-09-847-946A-53	Sequence 53, Appl
30	5	83.3	9	10	US-09-847-946A-54	Sequence 54, Appl
31	5	83.3	9	10	US-09-847-946A-58	Sequence 58, Appl
32	5	83.3	9	10	US-09-847-946A-61	Sequence 61, Appl
33	5	83.3	9	10	US-09-847-946A-64	Sequence 64, Appl
34	5	83.3	9	10	US-09-847-946A-65	Sequence 65, Appl
35	5	83.3	10	10	US-09-847-946A-49	Sequence 49, Appl
36	5	83.3	10	10	US-09-847-946A-52	Sequence 52, Appl
37	5	83.3	10	10	US-09-847-946A-57	Sequence 57, Appl
38	5	83.3	10	10	US-09-847-946A-60	Sequence 60, Appl
39	5	83.3	10	10	US-09-847-946A-63	Sequence 63, Appl
40	5	83.3	11	10	US-09-847-946A-46	Sequence 46, Appl
41	5	83.3	147	12	US-10-424-599-199086	Sequence 199086,
42	5	83.3	174	14	US-10-219-220-163	Sequence 163, App
43	5	83.3	225	14	US-10-219-220-162	Sequence 162, App
44	5	83.3	236	12	US-10-441-625-17	Sequence 17, Appl
45	5	83.3	236	14	US-10-441-626-17	Sequence 17, Appl
46	5	83.3	277	14	US-10-219-220-280	Sequence 280, App
47	5	83.3	312	14	US-10-306-762-23	Sequence 23, Appl
48	5	83.3	378	14	US-10-219-220-158	Sequence 158, App
49	5	83.3	501	14	US-10-171-311-234	Sequence 234, App
50	5	83.3	605	14	US-10-156-761-9070	Sequence 9070, Ap
51	5	83.3	5435	16	US-10-203-295-38	Sequence 38, Appl
52	4	66.7	6	9	US-09-847-940B-2	Sequence 2, Appli
53	4	66.7	6	10	US-09-847-946A-2	Sequence 2, Appli
54	4	66.7	6	10	US-09-847-946A-33	Sequence 33, Appl
55	4	66.7	7	10	US-09-847-946A-37	Sequence 37, Appl
56	4	66.7	8	10	US-09-847-946A-30	Sequence 30, Appl
57	4	66.7	8	10	US-09-847-946A-38	Sequence 38, Appl
58	4	66.7	9	10	US-09-847-946A-29	Sequence 29, Appl
59	4	66.7	9	10	US-09-847-946A-32	Sequence 32, Appl
60	4	66.7	9	10	US-09-847-946A-35	Sequence 35, Appl
61	4	66.7	9	10	US-09-847-946A-36	Sequence 36, Appl
62	4	66.7	10	10	US-09-847-946A-31	Sequence 31, Appl
63	4	66.7	10	10	US-09-847-946A-34	Sequence 34, Appl
64	4	66.7	11	10	US-09-847-946A-28	Sequence 28, Appl
65	4	66.7	11	10	US-09-847-946A-132	Sequence 132, App
66	4	66.7	11	10	US-09-847-946A-140	Sequence 140, App
67	4	66.7	12	10	US-09-847-946A-43	Sequence 43, Appl
68	4	66.7	12	10	US-09-954-385-340	Sequence 340, App
69	4	66.7	13	10	US-09-847-946A-143	Sequence 143, App
70	4	66.7	13	10	US-09-847-946A-144	Sequence 144, App
71	4	66.7	13	10	US-09-847-946A-145	Sequence 145, App
72	4	66.7	13	10	US-09-847-946A-148	Sequence 148, App
73	4	66.7	17	10	US-09-847-946A-141	Sequence 141, App
74	4	66.7	17	10	US-09-847-946A-142	Sequence 142, App
75	4	66.7	17	10	US-09-847-946A-146	Sequence 146, App
76	4	66.7	17	10	US-09-847-946A-147	Sequence 147, App
77	4	66.7	18	10	US-09-847-946A-131	Sequence 131, App
78	4	66.7	18	10	US-09-847-946A-135	Sequence 135, App
79	4	66.7	18	10	US-09-847-946A-136	Sequence 136, App
80	4	66.7	21	12	US-10-609-217-866	Sequence 866, App
81	4	66.7	21	12	US-10-632-388-866	Sequence 866, App
82	4	66.7	21	12	US-10-651-723-866	Sequence 866, App
83	4	66.7	21	12	US-10-645-761-866	Sequence 866, App
84	4	66.7	21	16	US-10-666-696-866	Sequence 866, App
85	4	66.7	21	16	US-10-653-048-866	Sequence 866, App
86	4	66.7	22	10	US-09-847-946A-133	Sequence 133, App
87	4	66.7	22	10	US-09-847-946A-134	Sequence 134, App
88	4	66.7	22	10	US-09-847-946A-137	Sequence 137, App

89	4	66.7	22	10	US-09-847-946A-138	Sequence 138, App	162	4	66.7	99	10	US-09-764-891-3660	Sequence 3660, Ap
90	4	66.7	22	10	US-09-847-946A-139	Sequence 139, App	163	4	66.7	101	15	US-10-094-749-2322	Sequence 2322, Ap
91	4	66.7	22	12	US-09-974-131A-12	Sequence 12, Appl	164	4	66.7	105	15	US-10-108-260A-4429	Sequence 4429, Ap
92	4	66.7	22	14	US-10-120-604-57	Sequence 57, Appl	165	4	66.7	106	12	US-10-424-599-211159	Sequence 211159,
93	4	66.7	22	14	US-10-278-314-12	Sequence 12, Appl	166	4	66.7	106	12	US-10-424-599-262413	Sequence 262413,
94	4	66.7	25	9	US-09-864-761-46354	Sequence 46354, A	167	4	66.7	114	15	US-10-264-237-2077	Sequence 2077, Ap
95	4	66.7	26	9	US-09-814-452-21	Sequence 21, Appl	168	4	66.7	115	12	US-10-220-120-321	Sequence 321, App
96	4	66.7	28	9	US-09-847-940B-18	Sequence 18, Appl	169	4	66.7	116	12	US-10-424-599-192081	Sequence 192081,
97	4	66.7	28	10	US-09-847-946A-18	Sequence 18, Appl	170	4	66.7	117	10	US-09-809-391-360	Sequence 360, App
98	4	66.7	28	12	US-10-602-303-2	Sequence 2, Appli	171	4	66.7	117	10	US-09-882-171-360	Sequence 360, App
99	4	66.7	29	10	US-09-962-756-1410	Sequence 1410, Ap	172	4	66.7	117	12	US-10-424-599-228673	Sequence 228673,
100	4	66.7	29	15	US-10-253-471-1410	Sequence 1410, Ap	173	4	66.7	117	12	US-10-164-861-360	Sequence 360, App
101	4	66.7	29	16	US-10-253-493-1410	Sequence 1410, Ap	174	4	66.7	117	15	US-10-108-260A-2639	Sequence 2639, Ap
102	4	66.7	36	9	US-09-814-452-3	Sequence 3, Appli	175	4	66.7	118	16	US-10-437-963-199154	Sequence 199154,
103	4	66.7	36	10	US-09-962-756-1320	Sequence 1320, Ap	176	4	66.7	119	15	US-10-104-047-3261	Sequence 3261, Ap
104	4	66.7	36	15	US-10-253-471-1320	Sequence 1320, Ap	177	4	66.7	119	16	US-10-389-566-475	Sequence 475, App
105	4	66.7	36	16	US-10-253-493-1320	Sequence 1320, Ap	178	4	66.7	120	16	US-10-437-963-118076	Sequence 118076,
106	4	66.7	37	9	US-09-814-452-1	Sequence 1, Appli	179	4	66.7	120	16	US-10-437-963-137856	Sequence 137856,
107	4	66.7	40	12	US-10-424-599-169200	Sequence 169200,	180	4	66.7	121	16	US-10-437-963-115821	Sequence 115821,
108	4	66.7	45	9	US-09-864-761-41236	Sequence 41236, A	181	4	66.7	122	14	US-10-106-698-4707	Sequence 4707, Ap
109	4	66.7	51	16	US-10-109-048-1087	Sequence 1087, Ap	182	4	66.7	122	15	US-10-104-047-3935	Sequence 3935, Ap
110	4	66.7	51	16	US-10-109-048-1088	Sequence 1088, Ap	183	4	66.7	123	16	US-10-437-963-117147	Sequence 117147,
111	4	66.7	51	16	US-10-109-048-1093	Sequence 1093, Ap	184	4	66.7	125	12	US-10-424-599-143106	Sequence 143106,
112	4	66.7	52	16	US-10-109-048-1085	Sequence 1085, Ap	185	4	66.7	125	16	US-10-437-963-119236	Sequence 119236,
113	4	66.7	52	16	US-10-109-048-1086	Sequence 1086, Ap	186	4	66.7	126	15	US-10-108-260A-2502	Sequence 2502, Ap
114	4	66.7	52	16	US-10-109-048-1090	Sequence 1090, Ap	187	4	66.7	127	12	US-10-425-114-40528	Sequence 40528, A
115	4	66.7	52	16	US-10-109-048-1091	Sequence 1091, Ap	188	4	66.7	128	14	US-10-279-029-105	Sequence 105, App
116	4	66.7	52	16	US-10-109-048-1092	Sequence 1092, Ap	189	4	66.7	129	16	US-10-437-963-108791	Sequence 108791,
117	4	66.7	52	16	US-10-109-048-1094	Sequence 1094, Ap	190	4	66.7	132	16	US-10-437-963-137466	Sequence 137466,
118	4	66.7	55	9	US-09-814-452-13	Sequence 13, Appl	191	4	66.7	133	12	US-10-424-599-207797	Sequence 207797,
119	4	66.7	56	9	US-09-814-452-11	Sequence 11, Appl	192	4	66.7	135	11	US-09-864-408A-6096	Sequence 6096, Ap
120	4	66.7	57	16	US-10-437-963-116410	Sequence 116410,	193	4	66.7	136	12	US-10-424-599-279912	Sequence 279912,
121	4	66.7	61	9	US-09-796-692-1003	Sequence 1003, Ap	194	4	66.7	136	12	US-10-424-599-284094	Sequence 284094,
122	4	66.7	61	14	US-10-040-862-1003	Sequence 1003, Ap	195	4	66.7	138	16	US-10-437-963-128107	Sequence 128107,
123	4	66.7	61	15	US-10-057-475B-1003	Sequence 1003, Ap	196	4	66.7	140	9	US-09-764-864-1379	Sequence 1379, Ap
124	4	66.7	61	15	US-10-154-884B-1003	Sequence 1003, Ap	197	4	66.7	144	12	US-10-282-122A-46942	Sequence 46942, A
125	4	66.7	61	16	US-10-437-963-146948	Sequence 146948,	198	4	66.7	144	14	US-10-101-464A-739	Sequence 739, App
126	4	66.7	63	12	US-10-424-599-208480	Sequence 208480,	199	4	66.7	146	12	US-10-282-122A-46540	Sequence 46540, A
127	4	66.7	63	12	US-10-424-599-239824	Sequence 239824,	200	4	66.7	148	12	US-10-424-599-212992	Sequence 212992,
128	4	66.7	64	12	US-10-424-599-273932	Sequence 273932,	201	4	66.7	149	12	US-10-424-599-157816	Sequence 157816,
129	4	66.7	66	12	US-10-424-599-207854	Sequence 207854,	202	4	66.7	149	12	US-10-424-599-263312	Sequence 263312,
130	4	66.7	67	10	US-09-764-891-3595	Sequence 3595, Ap	203	4	66.7	150	16	US-10-437-963-139014	Sequence 139014,
131	4	66.7	68	16	US-10-437-963-160449	Sequence 160449,	204	4	66.7	151	9	US-09-796-692-690	Sequence 690, App
132	4	66.7	68	16	US-10-437-963-196147	Sequence 196147,	205	4	66.7	151	14	US-10-040-862-690	Sequence 690, App
133	4	66.7	71	12	US-10-424-599-192697	Sequence 192697,	206	4	66.7	151	15	US-10-057-475B-690	Sequence 690, App
134	4	66.7	72	16	US-10-437-963-134351	Sequence 134351,	207	4	66.7	151	15	US-10-154-884B-690	Sequence 690, App
135	4	66.7	73	16	US-10-437-963-155224	Sequence 155224,	208	4	66.7	153	9	US-09-925-301-1367	Sequence 1367, Ap
136	4	66.7	74	12	US-10-424-599-149447	Sequence 149447,	209	4	66.7	155	12	US-10-425-114-39069	Sequence 39069, A
137	4	66.7	74	14	US-10-106-698-7099	Sequence 7099, Ap	210	4	66.7	160	12	US-10-282-122A-68173	Sequence 68173, A
138	4	66.7	75	16	US-10-109-048-1150	Sequence 1150, Ap	211	4	66.7	161	16	US-10-437-963-157766	Sequence 157766,
139	4	66.7	76	12	US-10-424-599-251348	Sequence 251348,	212	4	66.7	163	9	US-09-840-479-13	Sequence 13, Appl
140	4	66.7	78	9	US-09-071-838-184	Sequence 184, App	213	4	66.7	163	13	US-10-078-929-202	Sequence 202, App
141	4	66.7	78	12	US-10-425-114-42667	Sequence 42667, A	214	4	66.7	167	12	US-10-220-120-419	Sequence 419, App
142	4	66.7	78	14	US-10-213-512-184	Sequence 184, App	215	4	66.7	168	15	US-10-094-749-1806	Sequence 1806, Ap
143	4	66.7	78	16	US-10-437-963-189019	Sequence 189019,	216	4	66.7	170	10	US-09-975-719-339	Sequence 339, App
144	4	66.7	80	12	US-10-424-599-255598	Sequence 255598,	217	4	66.7	170	12	US-10-087-192-1047	Sequence 1047, Ap
145	4	66.7	82	11	US-09-833-245-1600	Sequence 1600, Ap	218	4	66.7	173	12	US-10-424-599-222161	Sequence 222161,
146	4	66.7	82	12	US-10-424-599-263066	Sequence 263066,	219	4	66.7	174	16	US-10-437-963-194553	Sequence 194553,
147	4	66.7	82	16	US-10-437-963-137643	Sequence 137643,	220	4	66.7	178	12	US-10-282-122A-66851	Sequence 66851, A
148	4	66.7	84	12	US-10-425-114-37259	Sequence 37259, A	221	4	66.7	179	16	US-10-437-963-132349	Sequence 132349,
149	4	66.7	86	12	US-09-978-360A-584	Sequence 584, App	222	4	66.7	180	16	US-10-437-963-185888	Sequence 185888,
150	4	66.7	88	12	US-10-424-599-210535	Sequence 210535,	223	4	66.7	181	14	US-10-156-761-11638	Sequence 11638, A
151	4	66.7	88	12	US-10-424-599-273840	Sequence 273840,	224	4	66.7	182	12	US-10-425-114-57909	Sequence 57909, A
152	4	66.7	90	12	US-10-424-599-249015	Sequence 249015,	225	4	66.7	188	12	US-10-425-114-47742	Sequence 47742, A
153	4	66.7	90	12	US-10-424-599-261138	Sequence 261138,	226	4	66.7	190	12	US-09-978-360A-488	Sequence 488, App
154	4	66.7	92	14	US-10-029-386-29710	Sequence 29710, A	227	4	66.7	190	12	US-09-978-360A-594	Sequence 594, App
155	4	66.7	93	12	US-10-424-599-229124	Sequence 229124,	228	4	66.7	195	12	US-10-425-114-71389	Sequence 71389, A
156	4	66.7	94	9	US-09-864-761-41701	Sequence 41701, A	229	4	66.7	195	15	US-10-094-749-3275	Sequence 3275, Ap
157	4	66.7	94	12	US-10-424-599-261839	Sequence 261839,	230	4	66.7	201	14	US-10-156-761-8837	Sequence 8837, Ap
158	4	66.7	95	12	US-10-424-599-167617	Sequence 167617,	231	4	66.7	201	16	US-10-437-963-104821	Sequence 104821,
159	4	66.7	96	16	US-10-437-963-139350	Sequence 139350,	232	4	66.7	202	12	US-10-424-599-150612	Sequence 150612,
160	4	66.7	97	16	US-10-437-963-150667	Sequence 150667,	233	4	66.7	202	15	US-10-104-047-2736	Sequence 2736, Ap
161	4	66.7	98	10	US-09-764-891-4516	Sequence 4516, Ap	234	4	66.7	204	12	US-10-424-599-182523	Sequence 182523,

Sequence 3660, Ap	Sequence 2322, Ap	Sequence 4429, Ap	Sequence 211159,	Sequence 262413,	Sequence 2077, Ap	Sequence 321, App	Sequence 192081,	Sequence 360, App	Sequence 360, App	Sequence 228673,	Sequence 360, App	Sequence 2639, Ap	Sequence 199154,	Sequence 3261, Ap	Sequence 475, App	Sequence 118076,	Sequence 137856,	Sequence 115821,	Sequence 4707, Ap	Sequence 3935, Ap	Sequence 117147,	Sequence 143106,	Sequence 119236,	Sequence 2502, Ap	Sequence 40528, A	Sequence 105, App	Sequence 108791,	Sequence 137466,	Sequence 207797,	Sequence 6096, Ap	Sequence 279912,	Sequence 284094,	Sequence 128107,	Sequence 1379, Ap	Sequence 46942, A	Sequence 739, App	Sequence 46540, A	Sequence 212992,	Sequence 157816,	Sequence 263312,	Sequence 139014,	Sequence 690, App	Sequence 690, App	Sequence 690, App	Sequence 690, App	Sequence 1367, Ap	Sequence 39069, A	Sequence 68173, A	Sequence 157766,	Sequence 13, Appl	Sequence 202, App	Sequence 419, App	Sequence 1806, Ap	Sequence 339, App	Sequence 1047, Ap	Sequence 222161,	Sequence 194553,	Sequence 66851, A	Sequence 132349,	Sequence 185888,	Sequence 11638, A	Sequence 57909, A	Sequence 47742, A	Sequence 488, App	Sequence 594, App	Sequence 71389, A	Sequence 3275, Ap	Sequence 8837, Ap	Sequence 104821,	Sequence 150612,	Sequence 2736, Ap	Sequence 182523,
-------------------	-------------------	-------------------	------------------	------------------	-------------------	-------------------	------------------	-------------------	-------------------	------------------	-------------------	-------------------	------------------	-------------------	-------------------	------------------	------------------	------------------	-------------------	-------------------	------------------	------------------	------------------	-------------------	-------------------	-------------------	------------------	------------------	------------------	-------------------	------------------	------------------	------------------	-------------------	-------------------	-------------------	-------------------	------------------	------------------	------------------	------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	------------------	------------------	-------------------	------------------	------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	------------------	------------------	-------------------	------------------

235	4	66.7	206	12	US-10-276-774-2422	Sequence 2422, Ap	308	4	66.7	293	15	US-10-374-780A-1565	Sequence 1565, Ap
236	4	66.7	207	12	US-10-424-599-170021	Sequence 170021,	309	4	66.7	293	16	US-10-437-963-151143	Sequence 151143,
237	4	66.7	210	15	US-10-264-049-3180	Sequence 3180, Ap	310	4	66.7	294	14	US-10-294-524-1	Sequence 1, Appli
238	4	66.7	212	14	US-10-319-799-69	Sequence 69, Appl	311	4	66.7	294	16	US-10-437-963-158062	Sequence 158062,
239	4	66.7	213	9	US-09-756-998-4	Sequence 4, Appli	312	4	66.7	295	12	US-10-425-114-50984	Sequence 50984, A
240	4	66.7	213	14	US-10-156-761-11043	Sequence 11043, A	313	4	66.7	295	14	US-10-316-253-271	Sequence 271, App
241	4	66.7	215	12	US-10-425-114-37563	Sequence 37563, A	314	4	66.7	296	16	US-10-437-963-183286	Sequence 183286,
242	4	66.7	215	12	US-10-425-114-62345	Sequence 62345, A	315	4	66.7	299	12	US-10-425-114-53040	Sequence 53040, A
243	4	66.7	217	16	US-10-437-963-142818	Sequence 142818,	316	4	66.7	300	14	US-10-306-762-80	Sequence 80, Appl
244	4	66.7	220	14	US-10-211-160-8	Sequence 8, Appli	317	4	66.7	300	16	US-10-437-963-123340	Sequence 123340,
245	4	66.7	220	14	US-10-051-681A-8	Sequence 8, Appli	318	4	66.7	301	12	US-10-425-114-52200	Sequence 52200, A
246	4	66.7	222	9	US-09-771-161A-141	Sequence 141, App	319	4	66.7	301	12	US-10-425-114-59716	Sequence 59716, A
247	4	66.7	224	15	US-10-264-049-2466	Sequence 2466, Ap	320	4	66.7	301	14	US-10-219-810-33	Sequence 33, Appl
248	4	66.7	225	12	US-10-282-122A-53684	Sequence 53684, A	321	4	66.7	301	14	US-10-219-810-34	Sequence 34, Appl
249	4	66.7	225	12	US-10-425-114-60752	Sequence 60752, A	322	4	66.7	305	14	US-10-219-810-38	Sequence 38, Appl
250	4	66.7	225	12	US-10-425-114-63074	Sequence 63074, A	323	4	66.7	306	9	US-09-866-572A-2	Sequence 2, Appli
251	4	66.7	228	16	US-10-437-963-186544	Sequence 186544,	324	4	66.7	306	9	US-09-866-570A-2	Sequence 2, Appli
252	4	66.7	232	12	US-10-425-114-37131	Sequence 37131, A	325	4	66.7	306	14	US-10-166-984-2	Sequence 2, Appli
253	4	66.7	232	14	US-10-156-761-10287	Sequence 10287, A	326	4	66.7	306	15	US-10-166-984-2	Sequence 2, Appli
254	4	66.7	232	14	US-10-156-761-11422	Sequence 11422, A	327	4	66.7	308	12	US-10-147-493-100	Sequence 100, App
255	4	66.7	234	15	US-10-369-493-7935	Sequence 7935, Ap	328	4	66.7	308	12	US-10-145-127-100	Sequence 100, App
256	4	66.7	235	16	US-10-437-963-167747	Sequence 167747,	329	4	66.7	308	12	US-10-160-503-100	Sequence 100, App
257	4	66.7	237	12	US-10-282-122A-60688	Sequence 60688, A	330	4	66.7	308	12	US-10-143-118-100	Sequence 100, App
258	4	66.7	238	12	US-10-441-625-15	Sequence 15, Appl	331	4	66.7	308	12	US-10-144-993-100	Sequence 100, App
259	4	66.7	238	14	US-10-441-626-15	Sequence 15, Appl	332	4	66.7	308	12	US-10-158-787-100	Sequence 100, App
260	4	66.7	239	12	US-10-425-114-68853	Sequence 68853, A	333	4	66.7	308	12	US-10-140-024-100	Sequence 100, App
261	4	66.7	239	12	US-10-441-625-7	Sequence 7, Appli	334	4	66.7	308	12	US-10-140-808-100	Sequence 100, App
262	4	66.7	239	14	US-10-441-626-7	Sequence 7, Appli	335	4	66.7	308	12	US-10-152-405-100	Sequence 100, App
263	4	66.7	243	12	US-10-425-114-70901	Sequence 70901, A	336	4	66.7	308	12	US-10-127-852A-100	Sequence 100, App
264	4	66.7	246	14	US-10-032-201B-188	Sequence 188, App	337	4	66.7	308	12	US-10-127-900A-100	Sequence 100, App
265	4	66.7	247	9	US-09-815-242-13461	Sequence 13461, A	338	4	66.7	308	12	US-10-128-685A-100	Sequence 100, App
266	4	66.7	247	9	US-09-815-242-13622	Sequence 13622, A	339	4	66.7	308	12	US-10-131-820A-100	Sequence 100, App
267	4	66.7	247	12	US-10-282-122A-72239	Sequence 72239, A	340	4	66.7	308	12	US-10-142-886-100	Sequence 100, App
268	4	66.7	249	12	US-10-282-122A-74775	Sequence 74775, A	341	4	66.7	308	12	US-10-146-728-100	Sequence 100, App
269	4	66.7	249	16	US-10-437-963-136538	Sequence 136538,	342	4	66.7	308	12	US-10-146-786-100	Sequence 100, App
270	4	66.7	249	16	US-10-437-963-200059	Sequence 200059,	343	4	66.7	308	12	US-10-147-499-100	Sequence 100, App
271	4	66.7	250	9	US-09-738-626-4799	Sequence 4799, Ap	344	4	66.7	308	12	US-10-157-798-100	Sequence 100, App
272	4	66.7	250	14	US-10-017-161-1662	Sequence 1662, Ap	345	4	66.7	308	14	US-10-028-072-100	Sequence 100, App
273	4	66.7	251	12	US-10-282-122A-74141	Sequence 74141, A	346	4	66.7	308	14	US-10-121-049-100	Sequence 100, App
274	4	66.7	251	16	US-10-437-963-123072	Sequence 123072,	347	4	66.7	308	14	US-10-123-904-100	Sequence 100, App
275	4	66.7	254	16	US-10-437-963-185711	Sequence 185711,	348	4	66.7	308	14	US-10-140-470-100	Sequence 100, App
276	4	66.7	255	12	US-10-282-122A-51101	Sequence 51101, A	349	4	66.7	308	14	US-10-175-746-100	Sequence 100, App
277	4	66.7	257	14	US-10-080-170-217	Sequence 217, App	350	4	66.7	308	14	US-10-176-918-100	Sequence 100, App
278	4	66.7	257	16	US-10-080-170-217	Sequence 217, App	351	4	66.7	308	14	US-10-176-921-100	Sequence 100, App
279	4	66.7	260	12	US-10-296-115-767	Sequence 767, App	352	4	66.7	308	14	US-10-137-865-100	Sequence 100, App
280	4	66.7	261	14	US-10-156-761-13812	Sequence 13812, A	353	4	66.7	308	14	US-10-140-474-100	Sequence 100, App
281	4	66.7	261	16	US-10-408-765A-1639	Sequence 1639, Ap	354	4	66.7	308	14	US-10-142-431-100	Sequence 100, App
282	4	66.7	261	16	US-10-437-963-172905	Sequence 172905,	355	4	66.7	308	14	US-10-143-114-100	Sequence 100, App
283	4	66.7	263	12	US-10-424-599-189338	Sequence 189338,	356	4	66.7	308	14	US-10-143-032-100	Sequence 100, App
284	4	66.7	263	16	US-10-437-963-145396	Sequence 145396,	357	4	66.7	308	14	US-10-142-419-100	Sequence 100, App
285	4	66.7	267	15	US-10-369-493-7929	Sequence 7929, Ap	358	4	66.7	308	14	US-10-123-262-100	Sequence 100, App
286	4	66.7	272	9	US-09-949-200B-1	Sequence 1, Appli	359	4	66.7	308	14	US-10-142-423-100	Sequence 100, App
287	4	66.7	273	12	US-10-282-122A-65381	Sequence 65381, A	360	4	66.7	308	14	US-10-121-050-100	Sequence 100, App
288	4	66.7	273	12	US-10-282-122A-66085	Sequence 66085, A	361	4	66.7	308	14	US-10-141-755-100	Sequence 100, App
289	4	66.7	276	12	US-10-424-599-143673	Sequence 143673,	362	4	66.7	308	14	US-10-143-032-100	Sequence 100, App
290	4	66.7	279	16	US-10-437-963-201282	Sequence 201282,	363	4	66.7	308	14	US-10-123-108-100	Sequence 100, App
291	4	66.7	280	9	US-09-712-363-283	Sequence 283, App	364	4	66.7	308	14	US-10-123-236-100	Sequence 100, App
292	4	66.7	280	12	US-10-389-647-371	Sequence 371, App	365	4	66.7	308	14	US-10-123-261-100	Sequence 100, App
293	4	66.7	280	14	US-10-279-029-106	Sequence 106, App	366	4	66.7	308	14	US-10-140-921-100	Sequence 100, App
294	4	66.7	280	14	US-10-279-029-107	Sequence 107, App	367	4	66.7	308	14	US-10-140-928-100	Sequence 100, App
295	4	66.7	280	14	US-10-219-810-39	Sequence 39, Appl	368	4	66.7	308	14	US-10-121-045-100	Sequence 100, App
296	4	66.7	280	14	US-10-219-810-40	Sequence 40, Appl	369	4	66.7	308	14	US-10-123-292-100	Sequence 100, App
297	4	66.7	281	14	US-10-211-160-10	Sequence 10, Appl	370	4	66.7	308	14	US-10-123-903-100	Sequence 100, App
298	4	66.7	281	14	US-10-051-681A-10	Sequence 10, Appl	371	4	66.7	308	14	US-10-124-819-100	Sequence 100, App
299	4	66.7	284	14	US-10-127-032-127	Sequence 127, App	372	4	66.7	308	14	US-10-124-822-100	Sequence 100, App
300	4	66.7	285	16	US-10-408-765A-2728	Sequence 2728, Ap	373	4	66.7	308	14	US-10-140-925-100	Sequence 100, App
301	4	66.7	286	14	US-10-259-165-208	Sequence 208, App	374	4	66.7	308	14	US-10-160-498-100	Sequence 100, App
302	4	66.7	286	15	US-10-369-493-18938	Sequence 18938, A	375	4	66.7	308	14	US-10-124-824-100	Sequence 100, App
303	4	66.7	289	16	US-10-437-963-154472	Sequence 154472,	376	4	66.7	308	14	US-10-127-825A-100	Sequence 100, App
304	4	66.7	292	12	US-10-425-114-59288	Sequence 59288, A	377	4	66.7	308	14	US-10-127-829A-100	Sequence 100, App
305	4	66.7	292	16	US-10-437-963-200200	Sequence 200200,	378	4	66.7	308	14	US-10-127-835A-100	Sequence 100, App
306	4	66.7	293	12	US-10-425-114-61999	Sequence 61999, A	379	4	66.7	308	14	US-10-127-839A-100	Sequence 100, App
307	4	66.7	293	14	US-10-306-762-178	Sequence 178, App	380	4	66.7	308	14	US-10-127-901A-100	Sequence 100, App

673	4	66.7	308	14	US-10-157-794-100	Sequence 100, App	746	4	66.7	308	15	US-10-140-809-100	Sequence 100, App
674	4	66.7	308	14	US-10-157-796-100	Sequence 100, App	747	4	66.7	308	15	US-10-140-865-100	Sequence 100, App
675	4	66.7	308	14	US-10-160-500-100	Sequence 100, App	748	4	66.7	308	15	US-10-141-701-100	Sequence 100, App
676	4	66.7	308	14	US-10-121-046-100	Sequence 100, App	749	4	66.7	308	15	US-10-141-754-100	Sequence 100, App
677	4	66.7	308	14	US-10-123-156-100	Sequence 100, App	750	4	66.7	308	15	US-10-141-760-100	Sequence 100, App
678	4	66.7	308	14	US-10-123-214-100	Sequence 100, App	751	4	66.7	308	15	US-10-142-425-100	Sequence 100, App
679	4	66.7	308	14	US-10-125-805-100	Sequence 100, App	752	4	66.7	308	15	US-10-142-430-100	Sequence 100, App
680	4	66.7	308	14	US-10-124-821-100	Sequence 100, App	753	4	66.7	308	15	US-10-143-113-100	Sequence 100, App
681	4	66.7	308	14	US-10-152-385-100	Sequence 100, App	754	4	66.7	308	15	US-10-146-730-100	Sequence 100, App
682	4	66.7	308	14	US-10-152-393-100	Sequence 100, App	755	4	66.7	308	15	US-10-146-792-100	Sequence 100, App
683	4	66.7	308	14	US-10-152-396-100	Sequence 100, App	756	4	66.7	308	15	US-10-158-791-100	Sequence 100, App
684	4	66.7	308	14	US-10-153-552-100	Sequence 100, App	757	4	66.7	308	15	US-10-156-843-100	Sequence 100, App
685	4	66.7	308	14	US-10-153-840-100	Sequence 100, App	758	4	66.7	308	15	US-10-157-786-100	Sequence 100, App
686	4	66.7	308	14	US-10-156-841-100	Sequence 100, App	759	4	66.7	308	15	US-10-147-528-100	Sequence 100, App
687	4	66.7	308	14	US-10-156-842-100	Sequence 100, App	760	4	66.7	308	15	US-10-128-692A-100	Sequence 100, App
688	4	66.7	308	14	US-10-156-844-100	Sequence 100, App	761	4	66.7	308	15	US-10-140-927-100	Sequence 100, App
689	4	66.7	308	14	US-10-156-845-100	Sequence 100, App	762	4	66.7	308	16	US-10-147-536-100	Sequence 100, App
690	4	66.7	308	14	US-10-156-846-100	Sequence 100, App	763	4	66.7	308	16	US-10-152-372-100	Sequence 100, App
691	4	66.7	308	14	US-10-121-048-100	Sequence 100, App	764	4	66.7	310	14	US-10-279-029-103	Sequence 103, App
692	4	66.7	308	14	US-10-121-052-100	Sequence 100, App	765	4	66.7	310	14	US-10-219-810-30	Sequence 30, Appl
693	4	66.7	308	14	US-10-121-053-100	Sequence 100, App	766	4	66.7	311	14	US-10-219-810-37	Sequence 37, Appl
694	4	66.7	308	14	US-10-121-054-100	Sequence 100, App	767	4	66.7	312	14	US-10-306-762-82	Sequence 82, Appl
695	4	66.7	308	14	US-10-121-063-100	Sequence 100, App	768	4	66.7	313	14	US-10-306-762-51	Sequence 51, Appl
696	4	66.7	308	14	US-10-123-212-100	Sequence 100, App	769	4	66.7	313	14	US-10-306-762-109	Sequence 109, App
697	4	66.7	308	14	US-10-123-213-100	Sequence 100, App	770	4	66.7	314	14	US-10-306-762-92	Sequence 92, Appl
698	4	66.7	308	14	US-10-123-291-100	Sequence 100, App	771	4	66.7	315	12	US-10-424-599-285456	Sequence 285456,
699	4	66.7	308	14	US-10-123-322-100	Sequence 100, App	772	4	66.7	317	10	US-09-880-729-2	Sequence 2, Appli
700	4	66.7	308	14	US-10-123-771-100	Sequence 100, App	773	4	66.7	317	14	US-10-219-810-41	Sequence 41, Appl
701	4	66.7	308	14	US-10-123-911-100	Sequence 100, App	774	4	66.7	319	9	US-09-738-626-3941	Sequence 3941, Ap
702	4	66.7	308	14	US-10-124-823-100	Sequence 100, App	775	4	66.7	319	12	US-10-425-114-69361	Sequence 69361, A
703	4	66.7	308	14	US-10-125-931-100	Sequence 100, App	776	4	66.7	319	14	US-10-032-585-7929	Sequence 7929, Ap
704	4	66.7	308	14	US-10-125-932-100	Sequence 100, App	777	4	66.7	320	14	US-10-306-762-235	Sequence 235, App
705	4	66.7	308	15	US-10-123-913-100	Sequence 100, App	778	4	66.7	321	12	US-10-424-599-239193	Sequence 239193,
706	4	66.7	308	15	US-10-140-473-100	Sequence 100, App	779	4	66.7	321	14	US-10-306-762-233	Sequence 233, App
707	4	66.7	308	15	US-10-140-806-100	Sequence 100, App	780	4	66.7	322	16	US-10-306-762-234	Sequence 234, App
708	4	66.7	308	15	US-10-140-810-100	Sequence 100, App	781	4	66.7	322	16	US-10-437-963-104913	Sequence 104913,
709	4	66.7	308	15	US-10-140-863-100	Sequence 100, App	782	4	66.7	323	16	US-10-647-196-12	Sequence 12, Appl
710	4	66.7	308	15	US-10-141-699-100	Sequence 100, App	783	4	66.7	325	12	US-10-282-122A-72165	Sequence 72165, A
711	4	66.7	308	15	US-10-141-703-100	Sequence 100, App	784	4	66.7	327	16	US-10-437-963-152954	Sequence 152954,
712	4	66.7	308	15	US-10-141-706-100	Sequence 100, App	785	4	66.7	328	12	US-10-072-012-514	Sequence 514, App
713	4	66.7	308	15	US-10-141-757-100	Sequence 100, App	786	4	66.7	329	12	US-10-424-599-166608	Sequence 166608,
714	4	66.7	308	15	US-10-141-762-100	Sequence 100, App	787	4	66.7	331	12	US-10-282-122A-56961	Sequence 56961, A
715	4	66.7	308	15	US-10-142-428-100	Sequence 100, App	788	4	66.7	333	9	US-09-764-870-279	Sequence 279, App
716	4	66.7	308	15	US-10-142-429-100	Sequence 100, App	789	4	66.7	333	14	US-10-125-540-279	Sequence 279, App
717	4	66.7	308	15	US-10-142-884-100	Sequence 100, App	790	4	66.7	334	14	US-10-156-761-11793	Sequence 11793, A
718	4	66.7	308	15	US-10-143-027-100	Sequence 100, App	791	4	66.7	336	9	US-09-815-242-13452	Sequence 13452, A
719	4	66.7	308	15	US-10-143-115-100	Sequence 100, App	792	4	66.7	336	12	US-10-282-122A-74153	Sequence 74153, A
720	4	66.7	308	15	US-10-144-956-100	Sequence 100, App	793	4	66.7	336	16	US-10-474-776-716	Sequence 716, App
721	4	66.7	308	15	US-10-144-958-100	Sequence 100, App	794	4	66.7	336	16	US-10-437-963-110311	Sequence 110311,
722	4	66.7	308	15	US-10-145-632-100	Sequence 100, App	795	4	66.7	337	9	US-09-861-289-14	Sequence 14, Appl
723	4	66.7	308	15	US-10-145-632-100	Sequence 100, App	796	4	66.7	337	9	US-09-860-846-14	Sequence 14, Appl
724	4	66.7	308	15	US-10-145-749-100	Sequence 100, App	797	4	66.7	337	10	US-09-988-384B-14	Sequence 14, Appl
725	4	66.7	308	15	US-10-145-753-100	Sequence 100, App	798	4	66.7	337	10	US-09-836-821-14	Sequence 14, Appl
726	4	66.7	308	15	US-10-145-871-100	Sequence 100, App	799	4	66.7	337	10	US-09-793-708-15	Sequence 15, Appl
727	4	66.7	308	15	US-10-145-878-100	Sequence 100, App	800	4	66.7	337	14	US-10-201-365-17	Sequence 15, Appl
728	4	66.7	308	15	US-10-146-794-100	Sequence 100, App	801	4	66.7	337	14	US-10-160-539-15	Sequence 15, Appl
729	4	66.7	308	15	US-10-147-489-100	Sequence 100, App	802	4	66.7	337	14	US-10-271-889-14	Sequence 14, Appl
730	4	66.7	308	15	US-10-147-507-100	Sequence 100, App	803	4	66.7	337	15	US-10-264-237-2527	Sequence 2527, Ap
731	4	66.7	308	15	US-10-147-535-100	Sequence 100, App	804	4	66.7	339	15	US-10-264-049-2718	Sequence 2718, Ap
732	4	66.7	308	15	US-10-147-537-100	Sequence 100, App	805	4	66.7	340	12	US-10-425-114-63326	Sequence 63326, A
733	4	66.7	308	15	US-10-152-376-100	Sequence 100, App	806	4	66.7	340	15	US-10-369-493-20435	Sequence 20435, A
734	4	66.7	308	15	US-10-152-381-100	Sequence 100, App	807	4	66.7	343	9	US-09-815-242-10844	Sequence 10844, A
735	4	66.7	308	15	US-10-152-400-100	Sequence 100, App	808	4	66.7	343	15	US-10-369-493-12342	Sequence 12342, A
736	4	66.7	308	15	US-10-153-585-100	Sequence 100, App	809	4	66.7	343	16	US-10-437-963-111769	Sequence 111769,
737	4	66.7	308	15	US-10-157-780-100	Sequence 100, App	810	4	66.7	345	12	US-10-425-114-53141	Sequence 53141, A
738	4	66.7	308	15	US-10-157-800-100	Sequence 100, App	811	4	66.7	345	16	US-10-229-148B-24	Sequence 24, Appl
739	4	66.7	308	15	US-10-157-801-100	Sequence 100, App	812	4	66.7	346	9	US-09-741-669-380	Sequence 380, App
740	4	66.7	308	15	US-10-157-802-100	Sequence 100, App	813	4	66.7	347	14	US-10-279-029-97	Sequence 97, Appl
741	4	66.7	308	15	US-10-158-784-100	Sequence 100, App	814	4	66.7	347	14	US-10-279-029-98	Sequence 98, Appl
742	4	66.7	308	15	US-10-158-789-100	Sequence 100, App	815	4	66.7	347	14	US-10-219-810-24	Sequence 24, Appl
743	4	66.7	308	15	US-10-192-011-100	Sequence 100, App	816	4	66.7	347	14	US-10-219-810-25	Sequence 25, Appl
744	4	66.7	308	15	US-10-139-963-100	Sequence 100, App	817	4	66.7	347	14	US-10-211-160-7	Sequence 7, Appli
745	4	66.7	308	15	US-10-140-020-100	Sequence 100, App	818	4	66.7	347	14	US-10-211-160-18	Sequence 18, Appl

819	4	66.7	347	14	US-10-051-681A-7	Sequence 7, Appli	892	4	66.7	432	15	US-10-369-493-3436	Sequence 3436, Ap
820	4	66.7	347	14	US-10-051-681A-18	Sequence 18, Appl	893	4	66.7	433	8	US-08-979-847-81	Sequence 81, Appl
821	4	66.7	347	15	US-10-369-493-17092	Sequence 17092, A	894	4	66.7	433	14	US-10-430-442-87	Sequence 87, Appl
822	4	66.7	347	15	US-10-240-145-167	Sequence 167, App	895	4	66.7	433	14	US-10-114-104-81	Sequence 81, Appl
823	4	66.7	347	16	US-10-408-765A-2146	Sequence 2146, Ap	896	4	66.7	434	12	US-10-282-122A-69137	Sequence 69137, A
824	4	66.7	348	14	US-10-279-029-91	Sequence 91, Appl	897	4	66.7	434	14	US-10-156-761-10099	Sequence 10099, A
825	4	66.7	348	14	US-10-279-029-92	Sequence 92, Appl	898	4	66.7	435	12	US-10-424-599-269483	Sequence 269483, A
826	4	66.7	348	14	US-10-219-810-18	Sequence 18, Appl	899	4	66.7	436	14	US-10-156-761-13899	Sequence 13899, A
827	4	66.7	348	14	US-10-219-810-19	Sequence 19, Appl	900	4	66.7	436	16	US-10-437-963-196797	Sequence 196797, A
828	4	66.7	348	14	US-10-342-224-26	Sequence 26, Appl	901	4	66.7	439	9	US-09-866-572A-28	Sequence 28, Appl
829	4	66.7	348	14	US-10-380-132-20	Sequence 20, Appl	902	4	66.7	439	9	US-09-866-570A-28	Sequence 28, Appl
830	4	66.7	348	16	US-10-471-243-24	Sequence 24, Appl	903	4	66.7	439	12	US-10-167-603C-12	Sequence 12, Appl
831	4	66.7	349	12	US-10-424-599-224877	Sequence 224877, A	904	4	66.7	439	14	US-10-166-984-28	Sequence 28, Appl
832	4	66.7	351	12	US-10-425-114-53701	Sequence 53701, A	905	4	66.7	439	15	US-10-369-493-9573	Sequence 9573, Ap
833	4	66.7	351	15	US-10-369-493-2738	Sequence 2738, Ap	906	4	66.7	439	15	US-10-166-984-28	Sequence 28, Appl
834	4	66.7	352	14	US-10-279-029-94	Sequence 94, Appl	907	4	66.7	440	14	US-10-156-761-9438	Sequence 9438, Ap
835	4	66.7	352	14	US-10-219-810-21	Sequence 21, Appl	908	4	66.7	440	14	US-10-204-887-141	Sequence 141, App
836	4	66.7	352	16	US-10-437-963-136554	Sequence 136554, A	909	4	66.7	441	12	US-10-424-599-186797	Sequence 186797, A
837	4	66.7	354	14	US-10-279-029-104	Sequence 104, App	910	4	66.7	441	12	US-10-424-599-190978	Sequence 190978, A
838	4	66.7	354	14	US-10-219-810-31	Sequence 31, Appl	911	4	66.7	441	12	US-10-425-114-55268	Sequence 55268, A
839	4	66.7	354	16	US-10-109-048-10	Sequence 10, Appl	912	4	66.7	442	12	US-10-425-114-58714	Sequence 58714, A
840	4	66.7	355	16	US-10-437-963-126020	Sequence 126020, A	913	4	66.7	444	14	US-10-112-488-40	Sequence 40, Appl
841	4	66.7	359	16	US-10-437-963-136865	Sequence 136865, A	914	4	66.7	444	16	US-10-437-963-191115	Sequence 191115, A
842	4	66.7	360	14	US-10-024-828-9	Sequence 9, Appli	915	4	66.7	447	12	US-10-282-122A-47761	Sequence 47761, A
843	4	66.7	361	12	US-10-425-114-62932	Sequence 62932, A	916	4	66.7	447	12	US-10-424-599-148178	Sequence 148178, A
844	4	66.7	362	12	US-10-425-114-40572	Sequence 40572, A	917	4	66.7	454	16	US-10-437-963-114396	Sequence 114396, A
845	4	66.7	362	12	US-10-425-114-72055	Sequence 72055, A	918	4	66.7	454	16	US-10-437-963-157725	Sequence 157725, A
846	4	66.7	362	12	US-10-425-114-72186	Sequence 72186, A	919	4	66.7	461	12	US-10-282-122A-52651	Sequence 52651, A
847	4	66.7	362	15	US-10-369-493-1617	Sequence 1617, Ap	920	4	66.7	462	16	US-10-437-963-111081	Sequence 111081, A
848	4	66.7	362	16	US-10-437-963-115286	Sequence 115286, A	921	4	66.7	464	12	US-10-282-122A-53392	Sequence 53392, A
849	4	66.7	364	14	US-10-279-029-93	Sequence 93, Appl	922	4	66.7	464	12	US-10-282-122A-60398	Sequence 60398, A
850	4	66.7	364	14	US-10-219-810-20	Sequence 20, Appl	923	4	66.7	464	15	US-10-369-493-4846	Sequence 4846, Ap
851	4	66.7	365	12	US-10-282-122A-53732	Sequence 53732, A	924	4	66.7	465	15	US-10-369-493-10682	Sequence 10682, A
852	4	66.7	366	16	US-10-437-963-153090	Sequence 153090, A	925	4	66.7	466	9	US-09-944-807-12	Sequence 12, Appl
853	4	66.7	371	12	US-10-424-599-179186	Sequence 179186, A	926	4	66.7	466	15	US-10-369-493-17472	Sequence 17472, A
854	4	66.7	371	15	US-10-369-493-8164	Sequence 8164, Ap	927	4	66.7	468	16	US-10-437-963-125823	Sequence 125823, A
855	4	66.7	374	12	US-10-424-599-150913	Sequence 150913, A	928	4	66.7	469	9	US-09-801-368-182	Sequence 182, App
856	4	66.7	374	12	US-10-425-114-49400	Sequence 49400, A	929	4	66.7	469	10	US-09-974-760B-41	Sequence 41, Appl
857	4	66.7	375	12	US-10-425-114-39448	Sequence 39448, A	930	4	66.7	469	10	US-09-974-760B-43	Sequence 43, Appl
858	4	66.7	378	15	US-10-369-493-12429	Sequence 12429, A	931	4	66.7	469	10	US-09-974-760B-44	Sequence 44, Appl
859	4	66.7	383	14	US-10-156-761-11368	Sequence 11368, A	932	4	66.7	469	10	US-09-974-760B-45	Sequence 45, Appl
860	4	66.7	384	14	US-10-156-761-9248	Sequence 9248, Ap	933	4	66.7	469	10	US-09-974-760B-46	Sequence 46, Appl
861	4	66.7	385	12	US-10-282-122A-68305	Sequence 68305, A	934	4	66.7	469	10	US-09-974-760B-47	Sequence 47, Appl
862	4	66.7	393	12	US-10-425-114-62682	Sequence 62682, A	935	4	66.7	469	10	US-09-974-760B-48	Sequence 48, Appl
863	4	66.7	395	16	US-10-437-963-147507	Sequence 147507, A	936	4	66.7	469	10	US-09-974-760B-49	Sequence 49, Appl
864	4	66.7	395	16	US-10-437-963-197095	Sequence 197095, A	937	4	66.7	469	10	US-09-974-760B-50	Sequence 50, Appl
865	4	66.7	396	12	US-10-282-122A-62153	Sequence 62153, A	938	4	66.7	469	10	US-09-974-760B-51	Sequence 51, Appl
866	4	66.7	397	16	US-10-437-963-187241	Sequence 187241, A	939	4	66.7	469	10	US-09-974-760B-52	Sequence 52, Appl
867	4	66.7	398	12	US-10-425-114-37491	Sequence 37491, A	940	4	66.7	469	10	US-09-974-760B-53	Sequence 53, Appl
868	4	66.7	399	12	US-10-425-114-45572	Sequence 45572, A	941	4	66.7	469	10	US-09-974-760B-54	Sequence 54, Appl
869	4	66.7	399	16	US-10-344-738-100	Sequence 100, App	942	4	66.7	469	10	US-09-974-760B-56	Sequence 56, Appl
870	4	66.7	400	14	US-10-156-761-11416	Sequence 11416, A	943	4	66.7	469	10	US-09-974-760B-57	Sequence 57, Appl
871	4	66.7	401	15	US-10-369-493-5805	Sequence 5805, Ap	944	4	66.7	469	10	US-09-974-760B-58	Sequence 58, Appl
872	4	66.7	402	16	US-10-467-433-5	Sequence 5, Appli	945	4	66.7	469	10	US-09-974-760B-59	Sequence 59, Appl
873	4	66.7	404	10	US-09-953-348-103	Sequence 103, App	946	4	66.7	469	10	US-09-974-760B-60	Sequence 60, Appl
874	4	66.7	404	12	US-10-425-114-52013	Sequence 52013, A	947	4	66.7	469	10	US-09-974-760B-61	Sequence 61, Appl
875	4	66.7	404	12	US-10-425-114-53828	Sequence 53828, A	948	4	66.7	469	10	US-09-974-760B-62	Sequence 62, Appl
876	4	66.7	404	14	US-10-267-255-103	Sequence 103, App	949	4	66.7	469	10	US-09-974-760B-63	Sequence 63, Appl
877	4	66.7	406	12	US-10-243-552-625	Sequence 625, App	950	4	66.7	469	10	US-09-974-760B-64	Sequence 64, Appl
878	4	66.7	414	12	US-10-425-114-70169	Sequence 70169, A	951	4	66.7	469	10	US-09-974-760B-91	Sequence 91, Appl
879	4	66.7	416	12	US-10-425-114-49276	Sequence 49276, A	952	4	66.7	469	16	US-10-149-310-154	Sequence 154, App
880	4	66.7	417	12	US-10-072-012-778	Sequence 778, App	953	4	66.7	470	10	US-09-974-760B-55	Sequence 55, Appl
881	4	66.7	420	12	US-10-425-114-72966	Sequence 72966, A	954	4	66.7	470	12	US-10-282-122A-52367	Sequence 52367, A
882	4	66.7	421	9	US-09-965-553-6	Sequence 6, Appli	955	4	66.7	470	14	US-10-156-761-10194	Sequence 10194, A
883	4	66.7	421	15	US-10-615-005-6	Sequence 6, Appli	956	4	66.7	474	12	US-10-374-903A-15	Sequence 15, Appl
884	4	66.7	421	15	US-10-395-607-6	Sequence 6, Appli	957	4	66.7	476	12	US-10-282-122A-75277	Sequence 75277, A
885	4	66.7	429	15	US-10-369-493-4176	Sequence 4176, Ap	958	4	66.7	477	12	US-10-072-012-777	Sequence 777, App
886	4	66.7	429	16	US-10-408-765A-1062	Sequence 1062, Ap	959	4	66.7	477	12	US-10-425-114-43312	Sequence 43312, A
887	4	66.7	429	16	US-10-437-963-129266	Sequence 129266, A	960	4	66.7	477	14	US-10-112-488-42	Sequence 42, Appl
888	4	66.7	430	16	US-10-437-963-120363	Sequence 120363, A	961	4	66.7	477	15	US-10-259-194A-2	Sequence 2, Appli
889	4	66.7	431	16	US-10-437-963-166478	Sequence 166478, A	962	4	66.7	477	16	US-10-673-860-10	Sequence 10, Appl
890	4	66.7	431	16	US-10-437-963-191114	Sequence 191114, A	963	4	66.7	478	16	US-10-389-566-1700	Sequence 1700, Ap
891	4	66.7	432	12	US-10-425-114-53665	Sequence 53665, A	964	4	66.7	482	14	US-10-156-761-12834	Sequence 12834, A

965	4	66.7	483	14	US-10-139-662-16	Sequence 16, Appl
966	4	66.7	483	14	US-10-139-683-16	Sequence 16, Appl
967	4	66.7	483	14	US-10-143-618-16	Sequence 16, Appl
968	4	66.7	483	15	US-10-369-493-11403	Sequence 11403, A
969	4	66.7	483	16	US-10-745-034-16	Sequence 16, Appl
970	4	66.7	484	9	US-09-815-242-10457	Sequence 10457, A
971	4	66.7	484	12	US-10-282-122A-56797	Sequence 56797, A
972	4	66.7	486	15	US-10-369-493-7605	Sequence 7605, Ap
973	4	66.7	486	16	US-10-437-963-118754	Sequence 118754,
974	4	66.7	489	10	US-09-888-320-2	Sequence 2, Appli
975	4	66.7	494	14	US-10-230-026-38	Sequence 38, Appl
976	4	66.7	495	11	US-09-833-245-302	Sequence 302, App
977	4	66.7	495	12	US-10-282-122A-68228	Sequence 68228, A
978	4	66.7	498	12	US-10-424-599-240738	Sequence 240738,
979	4	66.7	498	14	US-10-029-495-9	Sequence 9, Appli
980	4	66.7	498	15	US-10-369-493-8799	Sequence 8799, Ap
981	4	66.7	499	15	US-10-369-493-12666	Sequence 12666, A
982	4	66.7	500	12	US-10-425-114-56879	Sequence 56879, A
983	4	66.7	503	12	US-10-109-310-8	Sequence 8, Appli
984	4	66.7	503	15	US-10-369-493-13067	Sequence 13067, A
985	4	66.7	503	16	US-10-149-310-152	Sequence 152, App
986	4	66.7	503	16	US-10-437-963-125116	Sequence 125116,
987	4	66.7	506	15	US-10-369-493-17830	Sequence 17830, A
988	4	66.7	506	16	US-10-437-963-159885	Sequence 159885,
989	4	66.7	507	14	US-10-156-761-13988	Sequence 13988, A
990	4	66.7	508	15	US-10-369-493-14824	Sequence 14824, A
991	4	66.7	508	15	US-10-369-493-15014	Sequence 15014, A
992	4	66.7	514	11	US-09-907-421-10	Sequence 10, Appl
993	4	66.7	516	16	US-10-437-963-193217	Sequence 193217,
994	4	66.7	523	9	US-09-998-598-2603	Sequence 2603, Ap
995	4	66.7	523	14	US-10-029-495-3	Sequence 3, Appli
996	4	66.7	524	15	US-10-369-493-4784	Sequence 4784, Ap
997	4	66.7	524	15	US-10-369-493-7544	Sequence 7544, Ap
998	4	66.7	525	14	US-10-156-761-11016	Sequence 11016, A
999	4	66.7	527	15	US-10-369-493-6327	Sequence 6327, Ap
1000	4	66.7	534	14	US-10-156-761-8407	Sequence 8407, Ap

RESULT 1

US-09-847-946A-41

;

Sequence 41, Application US/09847946A

;

Publication No. US20030054999A1

;

GENERAL INFORMATION:

;

APPLICANT: May, Michael J

;

APPLICANT: Ghosh, Sankar

;

APPLICANT: Findeis, Mark A

;

APPLICANT: Phillips, Kathryn

;

APPLICANT: Hannig, Gerhard

;

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

;

FILE REFERENCE: PPI-119

;

CURRENT APPLICATION NUMBER: US/09/847,946A

;

CURRENT FILING DATE: 2001-05-02

;

PRIOR APPLICATION NUMBER: 60/201,261

;

PRIOR FILING DATE: 2000-05-02

;

PRIOR APPLICATION NUMBER: 09/643,260

;

PRIOR FILING DATE: 2000-08-22

;

NUMBER OF SEQ ID NOS: 160

;

SOFTWARE: PatentIn Ver. 2.0

;

SEQ ID NO 41

;

LENGTH: 6

;

TYPE: PRT

;

ORGANISM: Artificial Sequence

;

FEATURE:

;

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

;

OTHER INFORMATION: sequence

;

US-09-847-946A-41

Query Match

100.0%;

Score 6;

DB 10;

Length 6;

Best Local Similarity

100.0%;

Pred. No. 1.2e+06;

Matches

6;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

ALIGNMENTS

US-09-847-946A-41

US-09-847-946A-73

US-09-847-946A-77

Query Match

100.0%;

Score 6;

DB 10;

Length 6;

Best Local Similarity

100.0%;

Pred. No. 1.2e+06;

Matches

6;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

RESULT 2

US-09-847-946A-73

;

Sequence 73, Application US/09847946A

;

Publication No. US20030054999A1

;

GENERAL INFORMATION:

;

APPLICANT: May, Michael J

;

APPLICANT: Ghosh, Sankar

;

APPLICANT: Findeis, Mark A

;

APPLICANT: Phillips, Kathryn

;

APPLICANT: Hannig, Gerhard

;

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

;

FILE REFERENCE: PPI-119

;

CURRENT APPLICATION NUMBER: US/09/847,946A

;

CURRENT FILING DATE: 2001-05-02

;

PRIOR APPLICATION NUMBER: 60/201,261

;

PRIOR FILING DATE: 2000-05-02

;

PRIOR APPLICATION NUMBER: 09/643,260

;

PRIOR FILING DATE: 2000-08-22

;

NUMBER OF SEQ ID NOS: 160

;

SOFTWARE: PatentIn Ver. 2.0

;

SEQ ID NO 73

;

LENGTH: 6

;

TYPE: PRT

;

ORGANISM: Artificial Sequence

;

FEATURE:

;

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

;

OTHER INFORMATION: sequence

;

US-09-847-946A-73

Query Match

100.0%;

Score 6;

DB 10;

Length 6;

Best Local Similarity

100.0%;

Pred. No. 1.2e+06;

Matches

6;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

RESULT 3

US-09-847-946A-77

;

Sequence 77, Application US/09847946A

;

Publication No. US20030054999A1

;

GENERAL INFORMATION:

;

APPLICANT: May, Michael J

;

APPLICANT: Ghosh, Sankar

;

APPLICANT: Findeis, Mark A

;

APPLICANT: Phillips, Kathryn

;

APPLICANT: Hannig, Gerhard

;

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

;

FILE REFERENCE: PPI-119

;

CURRENT APPLICATION NUMBER: US/09/847,946A

;

CURRENT FILING DATE: 2001-05-02

;

PRIOR APPLICATION NUMBER: 60/201,261

;

PRIOR FILING DATE: 2000-05-02

;

PRIOR APPLICATION NUMBER: 09/643,260

;

PRIOR FILING DATE: 2000-08-22

;

NUMBER OF SEQ ID NOS: 160

;

SOFTWARE: PatentIn Ver. 2.0

;

SEQ ID NO 77

;

LENGTH: 7

;

TYPE: PRT

;

ORGANISM: Artificial Sequence

;

FEATURE:

;

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

;

OTHER INFORMATION: sequence

;

US-09-847-946A-77

Query Match

100.0%;

Score 6;

DB 10;

Length 6;

Best Local Similarity

100.0%;

Pred. No. 1.2e+06;

Matches

6;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Query Match 100.0%; Score 6; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 4
US-09-847-946A-70
; Sequence 70, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-70

Query Match 100.0%; Score 6; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 3 ADWSWA 8

RESULT 5
US-09-847-946A-78
; Sequence 78, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence
US-09-847-946A-78

Query Match 100.0%; Score 6; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 6
US-09-847-946A-69
; Sequence 69, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-69

Query Match 100.0%; Score 6; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 7
US-09-847-946A-72
; Sequence 72, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT


```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-72
Query Match      100.0%; Score 6; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      1 ADWSWA 6

RESULT 8
US-09-847-946A-75
; Sequence 75, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-75
Query Match      100.0%; Score 6; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      3 ADWSWA 8

RESULT 9
US-09-847-946A-76
; Sequence 76, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-76
Query Match      100.0%; Score 6; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      2 ADWSWA 7

RESULT 10
US-09-847-946A-71
; Sequence 71, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-71
Query Match      100.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      2 ADWSWA 7

RESULT 11
US-09-847-946A-74
; Sequence 74, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; SOFTWARE: PatentIn Ver. 2.0

```



```

; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-74

Query Match      100.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      3 ADWSWA 8

RESULT 12
US-09-847-946A-68
; Sequence 68, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-68

Query Match      100.0%; Score 6; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      3 ADWSWA 8

RESULT 13
US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-4

Query Match      83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      1 ADWSW 5

RESULT 14
US-09-847-940B-5
; Sequence 5, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-5

Query Match      83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      2 DWSWA 6

RESULT 15
US-09-847-946A-4
; Sequence 4, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
```



```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-51

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      1 ADWSW 5

RESULT 20
US-09-847-946A-62
; Sequence 62, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-62

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
Db      2 DWSWA 6

RESULT 21
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
```

```
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-55

Query Match      83.3%; Score 5; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      1 ADWSW 5

RESULT 22
US-09-847-946A-66
; Sequence 66, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-66

Query Match      83.3%; Score 5; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
Db      2 DWSWA 6

RESULT 23
US-09-847-946A-48
; Sequence 48, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
```



```

; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-48

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
      |||||
Db      3 ADWSW 7

RESULT 24
US-09-847-946A-56
; Sequence 56, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-56

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
      |||||
Db      1 ADWSW 5

RESULT 25
US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-59

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      4 DWSWA 8

RESULT 26
US-09-847-946A-67
; Sequence 67, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-67

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      2 DWSWA 6

RESULT 27
US-09-847-946A-47
; Sequence 47, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
```



```
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-47
```

```
Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ADWSW 5
        |||||
Db      1 ADWSW 5
```

RESULT 28

```
US-09-847-946A-50
; Sequence 50, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
```

```
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-50
```

```
Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ADWSW 5
        |||||
Db      1 ADWSW 5
```

RESULT 29

```
US-09-847-946A-53
; Sequence 53, Application US/09847946A
; Publication No. US20030054999A1
```

```
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-53
```

```
Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ADWSW 5
        |||||
Db      3 ADWSW 7
```

RESULT 30

```
US-09-847-946A-54
; Sequence 54, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
```

```
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-54
```

```
Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ADWSW 5
        |||||
Db      2 ADWSW 6
```

RESULT 31


```
US-09-847-946A-58
; Sequence 58, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-58

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      2 DWSWA 6

RESULT 32
US-09-847-946A-61
; Sequence 61, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-61

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      2 DWSWA 6

US-09-847-946A-65
; Sequence 65, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-65

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      2 DWSWA 6
```

```
RESULT 33
US-09-847-946A-64
; Sequence 64, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-64

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      4 DWSWA 8

RESULT 34
US-09-847-946A-65
; Sequence 65, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-65

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 2 DWSWA 6
|||||
Db 3 DWSWA 7

RESULT 35
US-09-847-946A-49
; Sequence 49, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-49

Query Match 83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 2 ADWSW 6

RESULT 36
US-09-847-946A-52
; Sequence 52, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-52

Query Match 83.3%; Score 5; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 3 ADWSW 7

RESULT 37
US-09-847-946A-57
; Sequence 57, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-57

Query Match 83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 3 DWSWA 7

RESULT 38
US-09-847-946A-60
; Sequence 60, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-60


```
US-09-847-946A-60
Query Match      83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      3 DWSWA 7

RESULT 39
US-09-847-946A-63
; Sequence 63, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-63

Query Match      83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      4 DWSWA 8

RESULT 40
US-09-847-946A-46
; Sequence 46, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-46

Query Match      83.3%; Score 5; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      3 ADWSW 7

RESULT 41
US-10-424-599-199086
; Sequence 199086, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199086
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2179C.1.pep
US-10-424-599-199086

Query Match      83.3%; Score 5; DB 12; Length 147;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      75 DWSWA 79

RESULT 42
US-10-219-220-163
; Sequence 163, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-163

Query Match      83.3%; Score 5; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
```



```

Db          109 ADWSW 113
          |||||
RESULT 43
US-10-219-220-162
; Sequence 162, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-162
Query Match      83.3%; Score 5; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 ADWSW 5
          |||||
Db          100 ADWSW 104

RESULT 44
US-10-441-625-17
; Sequence 17, Application US/10441625
; Publication No. US20030203467A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: Novel Variant EGI11-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,625
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-10-441-625-17
Query Match      83.3%; Score 5; DB 12; Length 236;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 ADWSW 5
          |||||
Db          63 ADWSW 67

RESULT 45
US-10-441-626-17
; Sequence 17, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
```

```

; TITLE OF INVENTION: No. US20030186418A1e1 Variant EGI11-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-10-441-626-17
Query Match      83.3%; Score 5; DB 14; Length 236;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 ADWSW 5
          |||||
Db          63 ADWSW 67

RESULT 46
US-10-219-220-280
; Sequence 280, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-280
Query Match      83.3%; Score 5; DB 14; Length 277;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 ADWSW 5
          |||||
Db          95 ADWSW 99

RESULT 47
US-10-306-762-23
; Sequence 23, Application US/10306762
; Publication No. US20030187220A1
; GENERAL INFORMATION:
; APPLICANT: Park, Frances
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
; TITLE OF INVENTION: MONONUCLEOTIDE BINDING PROTEIN (FMNBP)
; FILE REFERENCE: 52498-20011.00
; CURRENT APPLICATION NUMBER: US/10/306,762
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US 60/334,132
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 312
```



```
; TYPE: PRT
; ORGANISM: C. hutchinsonii (23137247)
US-10-306-762-23

Query Match      83.3%; Score 5; DB 14; Length 312;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      171 ADWSW 175

RESULT 48
US-10-219-220-158
; Sequence 158, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-158

Query Match      83.3%; Score 5; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      128 ADWSW 132

RESULT 49
US-10-171-311-234
; Sequence 234, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 234
; LENGTH: 501
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-234

Query Match      83.3%; Score 5; DB 14; Length 501;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      387 ADWSW 391

RESULT 50
US-10-156-761-9070
; Sequence 9070, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9070
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9070

Query Match      83.3%; Score 5; DB 14; Length 605;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      556 ADWSW 560

Search completed: July 23, 2004, 13:32:44
Job time : 43 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:25:00 ; Search time 19 Seconds
(without alignments)
16.303 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 6
Sequence: 1 ADWSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	83.3	68	4	US-09-252-991A-18367
2	5	83.3	142	4	US-09-252-991A-31533
3	5	83.3	174	4	US-09-325-932A-163
4	5	83.3	225	4	US-09-325-932A-162
5	5	83.3	236	4	US-09-632-570-17
6	5	83.3	236	4	US-09-632-575-47
7	5	83.3	242	4	US-09-345-236B-3
8	5	83.3	378	4	US-09-325-932A-158
9	5	83.3	445	4	US-09-252-991A-22368
10	5	83.3	462	4	US-09-252-991A-21704
11	4	66.7	5	6	5217869-75
12	4	66.7	8	1	US-08-435-925C-9
13	4	66.7	9	1	US-08-435-925C-10
14	4	66.7	21	1	US-08-190-788A-246
15	4	66.7	21	1	US-08-383-474B-249
16	4	66.7	21	1	US-08-465-391A-246
17	4	66.7	21	2	US-08-464-538B-246
18	4	66.7	21	2	US-08-463-076E-303
19	4	66.7	21	4	US-09-428-082B-866
20	4	66.7	44	3	US-08-905-223-274
21	4	66.7	74	1	US-08-379-538-2
22	4	66.7	78	3	US-09-177-249-184
23	4	66.7	79	4	US-09-252-991A-27207
24	4	66.7	80	4	US-09-621-976-4160
25	4	66.7	84	3	US-09-251-372-4
26	4	66.7	84	4	US-09-811-241-4
27	4	66.7	84	4	US-09-252-991A-19040
					Sequence 18367, A
					Sequence 31533, A
					Sequence 163, App
					Sequence 162, App
					Sequence 17, Appl
					Sequence 47, Appl
					Sequence 3, Appli
					Sequence 158, App
					Sequence 22368, A
					Sequence 21704, A
					Patent No. 5217869
					Sequence 9, Appli
					Sequence 10, Appl
					Sequence 246, App
					Sequence 249, App
					Sequence 246, App
					Sequence 246, App
					Sequence 303, App
					Sequence 866, App
					Sequence 274, App
					Sequence 2, Appli
					Sequence 184, App
					Sequence 27207, A
					Sequence 4160, App
					Sequence 4, Appli
					Sequence 19040, A

28	4	66.7	95	4	US-09-252-991A-31932	Sequence 31932, A
29	4	66.7	100	1	US-08-241-853-28	Sequence 28, Appl
30	4	66.7	100	1	US-08-241-853-29	Sequence 29, Appl
31	4	66.7	100	2	US-08-850-917-28	Sequence 28, Appl
32	4	66.7	100	2	US-08-850-917-29	Sequence 29, Appl
33	4	66.7	106	2	US-08-585-585A-4	Sequence 4, Appli
34	4	66.7	106	2	US-08-249-037C-4	Sequence 4, Appli
35	4	66.7	106	2	US-08-788-622B-4	Sequence 4, Appli
36	4	66.7	106	3	US-08-788-621B-4	Sequence 4, Appli
37	4	66.7	109	1	US-08-477-270-20	Sequence 20, Appl
38	4	66.7	117	4	US-09-149-476-360	Sequence 360, App
39	4	66.7	121	4	US-09-673-395A-204	Sequence 204, App
40	4	66.7	125	4	US-09-543-681A-7177	Sequence 7177, Ap
41	4	66.7	138	4	US-09-252-991A-20154	Sequence 20154, A
42	4	66.7	163	4	US-09-257-583-13	Sequence 13, Appl
43	4	66.7	164	4	US-09-252-991A-23817	Sequence 23817, A
44	4	66.7	170	4	US-09-199-637A-339	Sequence 339, App
45	4	66.7	172	4	US-09-252-991A-23876	Sequence 23876, A
46	4	66.7	189	4	US-09-252-991A-17160	Sequence 17160, A
47	4	66.7	191	4	US-09-252-991A-28753	Sequence 28753, A
48	4	66.7	191	4	US-09-134-000C-3705	Sequence 3705, Ap
49	4	66.7	197	4	US-09-489-039A-12525	Sequence 12525, A
50	4	66.7	201	4	US-09-540-236-2208	Sequence 2208, Ap
51	4	66.7	213	3	US-09-268-364-4	Sequence 4, Appli
52	4	66.7	213	4	US-09-252-991A-27051	Sequence 27051, A
53	4	66.7	217	4	US-09-107-532A-6250	Sequence 6250, Ap
54	4	66.7	218	4	US-09-252-991A-22136	Sequence 22136, A
55	4	66.7	227	4	US-09-252-991A-28338	Sequence 28338, A
56	4	66.7	227	4	US-09-489-039A-8752	Sequence 8752, Ap
57	4	66.7	234	4	US-09-252-991A-26682	Sequence 26682, A
58	4	66.7	234	4	US-09-252-991A-28300	Sequence 28300, A
59	4	66.7	238	4	US-09-632-570-15	Sequence 15, Appl
60	4	66.7	238	4	US-09-632-575-45	Sequence 45, Appl
61	4	66.7	239	3	US-09-216-295-7	Sequence 7, Appli
62	4	66.7	239	3	US-09-216-295-15	Sequence 15, Appl
63	4	66.7	239	4	US-09-632-570-7	Sequence 7, Appli
64	4	66.7	239	4	US-09-632-575-37	Sequence 37, Appl
65	4	66.7	246	3	US-08-634-475-3	Sequence 3, Appli
66	4	66.7	246	4	US-09-709-791-3	Sequence 3, Appli
67	4	66.7	247	4	US-08-858-207A-300	Sequence 300, App
68	4	66.7	250	4	US-09-252-991A-19161	Sequence 19161, A
69	4	66.7	253	4	US-09-252-991A-29646	Sequence 29646, A
70	4	66.7	262	3	US-08-634-475-2	Sequence 2, Appli
71	4	66.7	262	4	US-09-709-791-2	Sequence 2, Appli
72	4	66.7	262	4	US-09-489-039A-10584	Sequence 10584, A
73	4	66.7	268	4	US-09-252-991A-31998	Sequence 31998, A
74	4	66.7	272	4	US-09-107-532A-5541	Sequence 5541, Ap
75	4	66.7	273	4	US-09-252-991A-19592	Sequence 19592, A
76	4	66.7	278	4	US-09-134-000C-3724	Sequence 3724, Ap
77	4	66.7	289	4	US-09-120-051D-48	Sequence 48, Appl
78	4	66.7	289	4	US-09-120-051D-49	Sequence 49, Appl
79	4	66.7	298	1	US-08-095-726-4	Sequence 4, Appli
80	4	66.7	298	1	US-08-096-043-4	Sequence 4, Appli
81	4	66.7	298	1	US-08-093-577-4	Sequence 4, Appli
82	4	66.7	298	1	US-09-096-623A-4	Sequence 4, Appli
83	4	66.7	303	4	US-09-252-991A-28605	Sequence 28605, A
84	4	66.7	306	3	US-09-457-046B-2	Sequence 2, Appli
85	4	66.7	307	1	US-08-095-726-2	Sequence 2, Appli
86	4	66.7	307	1	US-08-096-043-2	Sequence 2, Appli
87	4	66.7	307	1	US-08-093-577-2	Sequence 2, Appli
88	4	66.7	307	1	US-08-096-623A-2	Sequence 2, Appli
89	4	66.7	309	4	US-09-252-991A-27944	Sequence 27944, A
90	4	66.7	316	4	US-09-252-991A-22454	Sequence 22454, A
91	4	66.7	317	2	US-09-066-075-2	Sequence 2, Appli
92	4	66.7	317	2	US-08-518-615A-2	Sequence 2, Appli
93	4	66.7	317	3	US-08-951-889-2	Sequence 2, Appli
94	4	66.7	317	3	US-09-472-857-2	Sequence 2, Appli
95	4	66.7	317	4	US-09-118-637A-2	Sequence 2, Appli
96	4	66.7	319	4	US-09-134-000C-6357	Sequence 6357, Ap
97	4	66.7	324	4	US-09-252-991A-24664	Sequence 24664, A
98	4	66.7	327	4	US-09-252-991A-26846	Sequence 26846, A
99	4	66.7	331	4	US-09-252-991A-18772	Sequence 18772, A
100	4	66.7	333	4	US-09-107-532A-4041	Sequence 4041, Ap

101	4	66.7	337	3	US-09-320-878-15	Sequence 15, Appl	174	4	66.7	715	3	US-08-458-731-10	Sequence 10, Appl
102	4	66.7	337	3	US-09-105-537-14	Sequence 14, Appl	175	4	66.7	715	3	US-08-149-223A-10	Sequence 10, Appl
103	4	66.7	337	4	US-09-141-908-17	Sequence 17, Appl	176	4	66.7	716	2	US-08-484-993B-14	Sequence 14, Appl
104	4	66.7	337	4	US-09-657-440-15	Sequence 15, Appl	177	4	66.7	716	2	US-08-484-158B-14	Sequence 14, Appl
105	4	66.7	345	4	US-09-134-000C-6382	Sequence 6382, Ap	178	4	66.7	716	2	US-08-484-596A-14	Sequence 14, Appl
106	4	66.7	348	1	US-07-989-845-2	Sequence 2, Appli	179	4	66.7	716	2	US-08-480-150A-14	Sequence 14, Appl
107	4	66.7	348	4	US-09-118-637A-4	Sequence 4, Appli	180	4	66.7	716	3	US-08-458-731-14	Sequence 14, Appl
108	4	66.7	348	5	PCT-US93-11298-2	Sequence 2, Appli	181	4	66.7	716	3	US-08-149-223A-14	Sequence 14, Appl
109	4	66.7	351	4	US-09-252-991A-25097	Sequence 25097, A	182	4	66.7	717	1	US-08-435-925C-2	Sequence 2, Appli
110	4	66.7	357	4	US-09-252-991A-20863	Sequence 20863, A	183	4	66.7	718	4	US-09-252-991A-25683	Sequence 25683, A
111	4	66.7	358	4	US-09-252-991A-16785	Sequence 16785, A	184	4	66.7	721	4	US-09-107-532A-6889	Sequence 6889, Ap
112	4	66.7	360	4	US-09-509-902A-9	Sequence 9, Appli	185	4	66.7	730	1	US-07-846-181-5	Sequence 5, Appli
113	4	66.7	389	4	US-09-252-991A-32389	Sequence 32389, A	186	4	66.7	730	1	US-07-845-989-5	Sequence 5, Appli
114	4	66.7	404	4	US-09-266-965-103	Sequence 103, App	187	4	66.7	735	4	US-09-252-991A-30246	Sequence 30246, A
115	4	66.7	408	4	US-09-489-039A-12523	Sequence 12523, A	188	4	66.7	745	2	US-08-887-518-3	Sequence 3, Appli
116	4	66.7	410	4	US-09-540-236-3584	Sequence 3584, Ap	189	4	66.7	745	2	US-09-023-321-3	Sequence 3, Appli
117	4	66.7	416	4	US-09-540-236-2565	Sequence 2565, Ap	190	4	66.7	745	2	US-08-890-853-4	Sequence 4, Appli
118	4	66.7	421	4	US-09-322-478-6	Sequence 6, Appli	191	4	66.7	745	2	US-09-032-475-3	Sequence 3, Appli
119	4	66.7	429	4	US-09-252-991A-22564	Sequence 22564, A	192	4	66.7	745	2	US-09-099-125A-4	Sequence 4, Appli
120	4	66.7	429	4	US-08-311-731A-68	Sequence 68, Appl	193	4	66.7	745	2	US-09-032-476-4	Sequence 4, Appli
121	4	66.7	433	3	US-08-691-563C-87	Sequence 87, Appl	194	4	66.7	745	3	US-08-890-854-4	Sequence 4, Appli
122	4	66.7	433	4	US-09-374-766-87	Sequence 87, Appl	195	4	66.7	745	3	US-09-023-324-4	Sequence 4, Appli
123	4	66.7	433	4	US-08-979-847B-81	Sequence 81, Appl	196	4	66.7	745	3	US-09-023-324-4	Sequence 4, Appli
124	4	66.7	438	4	US-09-252-991A-31307	Sequence 31307, A	197	4	66.7	745	3	US-09-168-629-2	Sequence 2, Appli
125	4	66.7	439	3	US-09-457-046B-28	Sequence 28, Appl	198	4	66.7	745	3	US-08-910-820-10	Sequence 10, Appl
126	4	66.7	440	4	US-09-543-681A-6033	Sequence 6033, Ap	199	4	66.7	745	3	US-08-810-131A-2	Sequence 2, Appli
127	4	66.7	445	4	US-09-252-991A-20277	Sequence 20277, A	200	4	66.7	745	4	US-09-109-986-4	Sequence 4, Appli
128	4	66.7	454	4	US-09-531-857A-4	Sequence 4, Appli	201	4	66.7	745	4	US-09-844-908-10	Sequence 10, Appl
129	4	66.7	474	4	US-08-311-731A-318	Sequence 318, App	202	4	66.7	745	4	US-09-868-758-3	Sequence 3, Appli
130	4	66.7	476	4	US-09-489-039A-8358	Sequence 8358, Ap	203	4	66.7	756	2	US-08-887-518-4	Sequence 4, Appli
131	4	66.7	480	4	US-09-252-991A-17687	Sequence 17687, A	204	4	66.7	756	2	US-09-023-321-4	Sequence 4, Appli
132	4	66.7	483	4	US-09-310-463-16	Sequence 16, Appl	205	4	66.7	756	2	US-08-890-853-2	Sequence 2, Appli
133	4	66.7	483	4	US-08-842-248A-16	Sequence 16, Appl	206	4	66.7	756	2	US-09-032-475-4	Sequence 4, Appli
134	4	66.7	487	4	US-09-252-991A-25447	Sequence 25447, A	207	4	66.7	756	2	US-09-099-125A-2	Sequence 2, Appli
135	4	66.7	487	4	US-09-489-039A-8887	Sequence 8887, Ap	208	4	66.7	756	2	US-09-099-124A-2	Sequence 2, Appli
136	4	66.7	503	4	US-09-215-694-8	Sequence 8, Appli	209	4	66.7	756	3	US-09-032-476-2	Sequence 2, Appli
137	4	66.7	506	4	US-09-252-991A-23066	Sequence 23066, A	210	4	66.7	756	3	US-08-890-854-2	Sequence 2, Appli
138	4	66.7	509	4	US-09-252-991A-20470	Sequence 20470, A	211	4	66.7	756	3	US-09-023-324-2	Sequence 2, Appli
139	4	66.7	526	2	US-08-852-401-3	Sequence 3, Appli	212	4	66.7	756	3	US-09-168-629-15	Sequence 15, Appl
140	4	66.7	542	4	US-09-252-991A-29987	Sequence 29987, A	213	4	66.7	756	3	US-08-910-820-9	Sequence 9, Appli
141	4	66.7	543	3	US-09-155-768-4	Sequence 4, Appli	214	4	66.7	756	4	US-09-109-986-2	Sequence 2, Appli
142	4	66.7	556	4	US-09-198-452A-596	Sequence 596, App	215	4	66.7	756	4	US-09-844-908-9	Sequence 9, Appli
143	4	66.7	570	4	US-09-565-501A-104	Sequence 104, App	216	4	66.7	756	4	US-09-868-758-4	Sequence 4, Appli
144	4	66.7	570	4	US-09-639-206A-104	Sequence 104, App	217	4	66.7	761	4	US-09-328-352-5942	Sequence 5942, Ap
145	4	66.7	570	4	US-09-874-923-104	Sequence 104, App	218	4	66.7	783	2	US-08-545-562A-5	Sequence 5, Appli
146	4	66.7	578	4	US-08-635-552A-2	Sequence 2, Appli	219	4	66.7	802	4	US-09-632-098-2	Sequence 2, Appli
147	4	66.7	581	4	US-09-252-991A-25414	Sequence 25414, A	220	4	66.7	826	4	US-09-134-000C-4999	Sequence 4999, Ap
148	4	66.7	583	4	US-08-675-499A-3	Sequence 3, Appli	221	4	66.7	828	4	US-09-543-681A-8171	Sequence 8171, Ap
149	4	66.7	583	4	US-08-812-008-3	Sequence 3, Appli	222	4	66.7	951	4	US-09-328-352-4456	Sequence 4456, Ap
150	4	66.7	586	3	US-08-964-268-3	Sequence 3, Appli	223	4	66.7	957	4	US-09-252-991A-30672	Sequence 30672, A
151	4	66.7	586	4	US-09-105-254-3	Sequence 2, Appli	224	4	66.7	968	4	US-09-751-389-6	Sequence 6, Appli
152	4	66.7	594	4	US-09-489-039A-10369	Sequence 10369, A	225	4	66.7	971	3	US-09-107-149-19	Sequence 19, Appl
153	4	66.7	596	3	US-09-135-232-2	Sequence 2, Appli	226	4	66.7	982	2	US-08-673-789-4	Sequence 4, Appli
154	4	66.7	596	4	US-09-863-549-2	Sequence 2, Appli	227	4	66.7	983	1	US-08-162-809-16	Sequence 16, Appl
155	4	66.7	604	2	US-08-756-317-6	Sequence 6, Appli	228	4	66.7	983	1	US-08-167-919A-10	Sequence 10, Appl
156	4	66.7	606	4	US-09-618-425-5	Sequence 5, Appli	229	4	66.7	983	2	US-08-449-645A-21	Sequence 21, Appl
157	4	66.7	608	4	US-09-489-039A-13204	Sequence 13204, A	230	4	66.7	983	2	US-08-702-367A-21	Sequence 21, Appl
158	4	66.7	616	3	US-09-136-574A-47	Sequence 47, Appl	231	4	66.7	983	3	US-08-715-106-10	Sequence 10, Appl
159	4	66.7	626	4	US-09-252-991A-21504	Sequence 21504, A	232	4	66.7	983	4	US-09-442-649-10	Sequence 10, Appl
160	4	66.7	626	4	US-09-800-729-95	Sequence 95, Appl	233	4	66.7	983	5	PCT-US95-04681-21	Sequence 21, Appl
161	4	66.7	630	4	US-09-107-532A-6830	Sequence 6830, Ap	234	4	66.7	996	4	US-09-417-197-123	Sequence 21, Appl
162	4	66.7	670	4	US-09-252-991A-22079	Sequence 22079, A	235	4	66.7	997	4	US-09-417-197-121	Sequence 10, Appl
163	4	66.7	671	3	US-09-121-321-16	Sequence 16, Appl	236	4	66.7	1001	1	US-07-797-556-6	Sequence 123, App
164	4	66.7	671	3	US-08-933-803A-16	Sequence 16, Appl	237	4	66.7	1001	1	US-07-943-843-2	Sequence 6, Appli
165	4	66.7	677	3	US-08-836-567-2	Sequence 2, Appli	238	4	66.7	1001	1	US-08-347-003-2	Sequence 2, Appli
166	4	66.7	677	3	US-09-606-304-2	Sequence 2, Appli	239	4	66.7	1036	3	US-08-968-752B-4	Sequence 4, Appli
167	4	66.7	689	3	US-09-177-249-2	Sequence 2, Appli	240	4	66.7	1036	4	US-09-536-224-4	Sequence 4, Appli
168	4	66.7	689	3	US-09-061-769A-2	Sequence 2, Appli	241	4	66.7	1043	4	US-09-536-224-4	Sequence 4, Appli
169	4	66.7	700	2	US-07-862-588B-2	Sequence 2, Appli	242	4	66.7	1047	4	US-09-252-991A-32210	Sequence 32210, A
170	4	66.7	715	2	US-08-484-993B-10	Sequence 10, Appl	243	4	66.7	1074	2	US-09-543-681A-6186	Sequence 6186, Ap
171	4	66.7	715	2	US-08-484-158B-10	Sequence 10, Appl	244	4	66.7	1074	3	US-08-768-147B-2	Sequence 2, Appli
172	4	66.7	715	2	US-08-484-596A-10	Sequence 10, Appl	245	4	66.7	1074	3	US-09-107-149-3	Sequence 2, Appli
173	4	66.7	715	2	US-08-480-150A-10	Sequence 10, Appl	246	4	66.7	1074	4	US-09-536-224-2	Sequence 3, Appli

247	4	66.7	1086	4	US-09-252-991A-25051	Sequence 25051, A	Sequence 25051, A	320	3	50.0	8	3	US-09-082-279B-1480	Sequence 1480, Ap
248	4	66.7	1097	1	US-07-943-843-6	Sequence 6, Appli	Sequence 6, Appli	321	3	50.0	8	3	US-09-082-279B-1482	Sequence 1482, Ap
249	4	66.7	1097	1	US-08-347-003-6	Sequence 6, Appli	Sequence 6, Appli	322	3	50.0	8	3	US-09-082-279B-1494	Sequence 1494, Ap
250	4	66.7	1170	4	US-09-638-524A-2	Sequence 2, Appli	Sequence 2, Appli	323	3	50.0	8	3	US-09-082-279B-1499	Sequence 1499, Ap
251	4	66.7	1180	4	US-09-252-991A-32464	Sequence 32464, A	Sequence 32464, A	324	3	50.0	8	3	US-09-082-279B-1502	Sequence 1502, Ap
252	4	66.7	1197	3	US-08-836-567-12	Sequence 12, Appl	Sequence 12, Appl	325	3	50.0	8	3	US-09-082-279B-1504	Sequence 1504, Ap
253	4	66.7	1197	4	US-09-606-304-12	Sequence 12, Appl	Sequence 12, Appl	326	3	50.0	8	3	US-09-082-279B-1506	Sequence 1506, Ap
254	4	66.7	1230	2	US-08-968-542C-35	Sequence 35, Appl	Sequence 35, Appl	327	3	50.0	8	3	US-09-082-279B-1507	Sequence 1507, Ap
255	4	66.7	1230	4	US-09-554-467A-35	Sequence 35, Appl	Sequence 35, Appl	328	3	50.0	8	3	US-09-082-279B-1511	Sequence 1511, Ap
256	4	66.7	1269	4	US-09-252-991A-23150	Sequence 23150, A	Sequence 23150, A	329	3	50.0	8	4	US-09-043-731-4	Sequence 4, Appli
257	4	66.7	1272	4	US-09-543-681A-5732	Sequence 5732, Ap	Sequence 5732, Ap	330	3	50.0	8	4	US-09-315-304B-1629	Sequence 1629, Ap
258	4	66.7	1426	3	US-09-136-574A-43	Sequence 43, Appl	Sequence 43, Appl	331	3	50.0	8	4	US-09-315-304B-1630	Sequence 1630, Ap
259	4	66.7	1674	2	US-08-968-542C-12	Sequence 12, Appl	Sequence 12, Appl	332	3	50.0	8	4	US-09-315-304B-1631	Sequence 1631, Ap
260	4	66.7	1674	4	US-09-554-467A-12	Sequence 12, Appl	Sequence 12, Appl	333	3	50.0	8	4	US-09-315-304B-1632	Sequence 1632, Ap
261	4	66.7	1751	3	US-09-136-574A-44	Sequence 44, Appl	Sequence 44, Appl	334	3	50.0	8	4	US-09-315-304B-1633	Sequence 1633, Ap
262	4	66.7	1841	2	US-08-804-227C-6	Sequence 6, Appli	Sequence 6, Appli	335	3	50.0	8	4	US-09-315-304B-1634	Sequence 1634, Ap
263	4	66.7	2482	4	US-09-252-991A-16967	Sequence 16967, A	Sequence 16967, A	336	3	50.0	8	4	US-09-315-304B-1636	Sequence 1636, Ap
264	4	66.7	3168	4	US-09-489-039A-14067	Sequence 14067, A	Sequence 14067, A	337	3	50.0	8	4	US-09-315-304B-1648	Sequence 1648, Ap
265	4	66.7	3782	3	US-09-105-537-4	Sequence 4, Appli	Sequence 4, Appli	338	3	50.0	8	4	US-09-315-304B-1653	Sequence 1653, Ap
266	4	66.7	4630	4	US-09-091-609-2	Sequence 2, Appli	Sequence 2, Appli	339	3	50.0	8	4	US-09-315-304B-1656	Sequence 1656, Ap
267	4	66.7	5215	3	US-09-105-537-2	Sequence 2, Appli	Sequence 2, Appli	340	3	50.0	8	4	US-09-315-304B-1658	Sequence 1658, Ap
268	3	50.0	4	2	US-08-478-386A-7	Sequence 7, Appli	Sequence 7, Appli	341	3	50.0	8	4	US-09-315-304B-1660	Sequence 1660, Ap
269	3	50.0	4	2	US-08-292-597-7	Sequence 7, Appli	Sequence 7, Appli	342	3	50.0	8	4	US-09-315-304B-1665	Sequence 1665, Ap
270	3	50.0	4	2	US-08-388-653-7	Sequence 7, Appli	Sequence 7, Appli	343	3	50.0	8	4	US-08-439-157-5	Sequence 5, Appli
271	3	50.0	4	2	US-08-473-985-7	Sequence 7, Appli	Sequence 7, Appli	344	3	50.0	8	4	US-08-439-157-34	Sequence 34, Appl
272	3	50.0	4	2	US-08-483-898-7	Sequence 7, Appli	Sequence 7, Appli	345	3	50.0	8	4	US-08-439-157-75	Sequence 75, Appl
273	3	50.0	4	3	US-08-689-421-9	Sequence 9, Appli	Sequence 9, Appli	346	3	50.0	8	4	US-09-437-895-5	Sequence 5, Appli
274	3	50.0	4	3	US-09-087-716-7	Sequence 7, Appli	Sequence 7, Appli	347	3	50.0	8	4	US-09-437-895-34	Sequence 34, Appl
275	3	50.0	4	3	US-08-297-395-68	Sequence 68, Appl	Sequence 68, Appl	348	3	50.0	8	4	US-09-437-895-75	Sequence 75, Appl
276	3	50.0	4	3	US-08-297-395-71	Sequence 71, Appl	Sequence 71, Appl	349	3	50.0	8	4	US-08-469-260A-528	Sequence 528, App
277	3	50.0	4	3	US-08-297-395-74	Sequence 74, Appl	Sequence 74, Appl	350	3	50.0	8	4	US-08-488-446-528	Sequence 528, App
278	3	50.0	4	3	US-09-157-753-7	Sequence 7, Appli	Sequence 7, Appli	351	3	50.0	8	4	US-09-834-784-1475	Sequence 1475, Ap
279	3	50.0	4	3	US-09-157-230-7	Sequence 7, Appli	Sequence 7, Appli	352	3	50.0	8	4	US-09-834-784-1476	Sequence 1476, Ap
280	3	50.0	4	3	US-09-087-811-7	Sequence 7, Appli	Sequence 7, Appli	353	3	50.0	8	4	US-09-834-784-1477	Sequence 1477, Ap
281	3	50.0	4	3	US-09-156-855-7	Sequence 7, Appli	Sequence 7, Appli	354	3	50.0	8	4	US-09-834-784-1479	Sequence 1479, Ap
282	3	50.0	4	3	US-09-158-010-7	Sequence 7, Appli	Sequence 7, Appli	355	3	50.0	8	4	US-09-834-784-1480	Sequence 1480, Ap
283	3	50.0	4	3	US-09-087-647-7	Sequence 7, Appli	Sequence 7, Appli	356	3	50.0	8	4	US-09-834-784-1482	Sequence 1482, Ap
284	3	50.0	4	3	US-09-389-528-9	Sequence 9, Appli	Sequence 9, Appli	357	3	50.0	8	4	US-09-834-784-1494	Sequence 1494, Ap
285	3	50.0	4	3	US-09-181-827A-9	Sequence 9, Appli	Sequence 9, Appli	358	3	50.0	8	4	US-09-834-784-1499	Sequence 1499, Ap
286	4	50.0	4	4	US-09-302-629-7	Sequence 7, Appli	Sequence 7, Appli	359	3	50.0	8	4	US-09-834-784-1502	Sequence 1502, Ap
287	3	50.0	5	2	US-08-684-687-7	Sequence 7, Appli	Sequence 7, Appli	360	3	50.0	8	4	US-09-834-784-1504	Sequence 1504, Ap
288	3	50.0	5	3	US-08-981-122-55	Sequence 55, Appl	Sequence 55, Appl	361	3	50.0	8	4	US-09-834-784-1506	Sequence 1506, Ap
289	3	50.0	5	6	5217869-56	Patent No. 5217869	Patent No. 5217869	362	3	50.0	8	4	US-09-834-784-1507	Sequence 1507, Ap
290	3	50.0	6	1	US-08-596-116A-3	Sequence 3, Appli	Sequence 3, Appli	363	3	50.0	8	4	US-09-834-784-1511	Sequence 1511, Ap
291	3	50.0	6	1	US-08-596-116A-6	Sequence 6, Appli	Sequence 6, Appli	364	3	50.0	8	4	US-08-467-344A-528	Sequence 528, App
292	3	50.0	6	1	US-08-596-116A-9	Sequence 9, Appli	Sequence 9, Appli	365	3	50.0	8	4	US-09-350-641C-1630	Sequence 1630, Ap
293	3	50.0	6	1	US-08-596-116A-13	Sequence 13, Appl	Sequence 13, Appl	366	3	50.0	8	4	US-09-350-641C-1631	Sequence 1631, Ap
294	3	50.0	6	1	US-08-596-116A-16	Sequence 16, Appl	Sequence 16, Appl	367	3	50.0	8	4	US-09-350-641C-1632	Sequence 1632, Ap
295	3	50.0	6	1	US-08-596-116A-21	Sequence 21, Appl	Sequence 21, Appl	368	3	50.0	8	4	US-09-350-641C-1634	Sequence 1634, Ap
296	3	50.0	6	1	US-08-596-116A-26	Sequence 26, Appl	Sequence 26, Appl	369	3	50.0	8	4	US-09-350-641C-1635	Sequence 1635, Ap
297	3	50.0	6	1	US-08-596-116A-29	Sequence 29, Appl	Sequence 29, Appl	370	3	50.0	8	4	US-09-350-641C-1637	Sequence 1637, Ap
298	3	50.0	6	1	US-08-596-116A-33	Sequence 33, Appl	Sequence 33, Appl	371	3	50.0	8	4	US-09-350-641C-1649	Sequence 1649, Ap
299	3	50.0	6	1	US-08-596-116A-42	Sequence 42, Appl	Sequence 42, Appl	372	3	50.0	8	4	US-09-350-641C-1654	Sequence 1654, Ap
300	3	50.0	6	4	US-08-981-957D-9	Sequence 9, Appli	Sequence 9, Appli	373	3	50.0	8	4	US-09-350-641C-1657	Sequence 1657, Ap
301	3	50.0	6	4	US-08-871-561-28	Sequence 28, Appl	Sequence 28, Appl	374	3	50.0	8	4	US-09-350-641C-1659	Sequence 1659, Ap
302	3	50.0	6	4	US-09-301-593-67	Sequence 67, Appl	Sequence 67, Appl	375	3	50.0	8	4	US-09-350-641C-1661	Sequence 1661, Ap
303	3	50.0	6	4	US-09-321-932B-28	Sequence 28, Appl	Sequence 28, Appl	376	3	50.0	8	4	US-09-350-641C-1662	Sequence 1662, Ap
304	3	50.0	6	6	5217891-1	Patent No. 5217891	Patent No. 5217891	377	3	50.0	8	4	US-09-350-641C-1666	Sequence 1666, Ap
305	3	50.0	7	1	US-07-801-812A-24	Sequence 24, Appl	Sequence 24, Appl	378	3	50.0	9	3	US-08-159-339A-340	Sequence 340, App
306	3	50.0	7	1	US-08-173-510B-77	Sequence 77, Appl	Sequence 77, Appl	379	3	50.0	9	3	US-09-258-754-350	Sequence 350, App
307	3	50.0	7	1	US-08-462-661A-46	Sequence 46, Appl	Sequence 46, Appl	380	3	50.0	9	3	US-09-042-107-350	Sequence 350, App
308	3	50.0	7	1	US-08-487-568-24	Sequence 24, Appl	Sequence 24, Appl	381	3	50.0	9	3	US-09-510-738A-45	Sequence 45, Appl
309	3	50.0	7	1	US-08-458-218-75	Sequence 75, Appl	Sequence 75, Appl	382	3	50.0	9	3	US-09-510-738A-105	Sequence 105, App
310	3	50.0	7	2	US-08-450-497-77	Sequence 77, Appl	Sequence 77, Appl	383	3	50.0	9	3	US-09-510-738A-106	Sequence 106, App
311	3	50.0	7	6	531899-62	Patent No. 531899	Patent No. 531899	384	3	50.0	9	3	US-09-510-738A-121	Sequence 121, App
312	3	50.0	8	3	US-08-336-553A-5	Sequence 5, Appli	Sequence 5, Appli	385	3	50.0	9	4	US-08-817-441-22	Sequence 22, Appl
313	3	50.0	8	3	US-08-336-553A-34	Sequence 34, Appl	Sequence 34, Appl	386	3	50.0	9	4	US-09-861-966-45	Sequence 45, Appl
314	3	50.0	8	3	US-08-336-553A-75	Sequence 75, Appl	Sequence 75, Appl	387	3	50.0	9	4	US-09-861-966-105	Sequence 105, App
315	3	50.0	8	3	US-08-444-818-377	Sequence 377, App	Sequence 377, App	388	3	50.0	9	4	US-09-861-966-106	Sequence 106, App
316	3	50.0	8	3	US-09-082-279B-1475	Sequence 1475, Ap	Sequence 1475, Ap	389	3	50.0	9	4	US-09-861-966-121	Sequence 121, App
317	3	50.0	8	3	US-09-082-279B-1476	Sequence 1476, Ap	Sequence 1476, Ap	390	3	50.0	9	4	US-09-311-784A-164	Sequence 164, App
318	3	50.0	8	3	US-09-082-279B-1477	Sequence 1477, Ap	Sequence 1477, Ap	391	3	50.0	9	4	US-09-311-784A-228	Sequence 228, App
319	3	50.0	8	3	US-09-082-279B-1479	Sequence 1479, Ap	Sequence 1479, Ap	392	3	50.0	9	4	US-09-311-784A-231	Sequence 231, App

393	3	50.0	9	4	US-09-311-784A-232	Sequence 232, App	466	3	50.0	19	1	US-08-290-448A-16	Sequence 16, Appl
394	3	50.0	9	4	US-09-311-784A-233	Sequence 233, App	467	3	50.0	19	1	US-08-290-448A-16	Sequence 16, Appl
395	3	50.0	9	4	US-09-722-250D-350	Sequence 350, App	468	3	50.0	19	1	US-08-471-033-25	Sequence 25, Appl
396	3	50.0	10	1	US-07-965-675-7	Sequence 7, Appli	469	3	50.0	19	1	US-08-484-635-104	Sequence 104, App
397	3	50.0	10	1	US-08-264-093-8	Sequence 8, Appli	470	3	50.0	19	1	US-08-175-069A-16	Sequence 16, Appl
398	3	50.0	10	1	US-08-290-448A-53	Sequence 53, Appl	471	3	50.0	19	2	US-08-484-631-104	Sequence 104, App
399	3	50.0	10	1	US-08-290-448A-53	Sequence 53, Appl	472	3	50.0	19	2	US-08-471-044-25	Sequence 25, Appl
400	3	50.0	10	1	US-08-175-069A-53	Sequence 53, Appl	473	3	50.0	19	2	US-08-463-483A-25	Sequence 25, Appl
401	3	50.0	10	2	US-08-726-464B-8	Sequence 8, Appli	474	3	50.0	19	2	US-08-471-046A-25	Sequence 25, Appl
402	3	50.0	10	2	US-08-726-464B-11	Sequence 11, Appl	475	3	50.0	19	2	US-08-470-566B-25	Sequence 25, Appl
403	3	50.0	10	3	US-08-159-339A-478	Sequence 478, App	476	3	50.0	19	2	US-08-827-570-104	Sequence 104, App
404	3	50.0	10	4	US-08-461-939B-53	Sequence 53, Appl	477	3	50.0	19	2	US-09-174-060-20	Sequence 20, Appl
405	3	50.0	10	4	US-08-464-000-53	Sequence 53, Appl	478	3	50.0	19	2	US-08-469-334-25	Sequence 25, Appl
406	3	50.0	10	4	US-09-790-497A-26	Sequence 26, Appl	479	3	50.0	19	3	US-09-300-529-25	Sequence 25, Appl
407	3	50.0	10	4	US-09-428-082B-37	Sequence 37, Appl	480	3	50.0	19	3	US-08-338-382-20	Sequence 20, Appl
408	3	50.0	10	5	PCT-US91-02942-61	Sequence 61, Appl	481	3	50.0	19	4	US-08-461-939B-16	Sequence 16, Appl
409	3	50.0	10	6	5198533-4	Patent No. 5198533	482	3	50.0	19	4	US-08-464-000-16	Sequence 16, Appl
410	3	50.0	10	6	5217891-20	Patent No. 5217891	483	3	50.0	19	4	US-08-469-260A-432	Sequence 432, App
411	3	50.0	11	2	US-08-849-536A-16	Sequence 16, Appl	484	3	50.0	19	4	US-09-301-593-61	Sequence 61, Appl
412	3	50.0	11	3	US-09-183-217-9	Sequence 9, Appli	485	3	50.0	19	4	US-08-488-446-432	Sequence 432, App
413	3	50.0	11	3	US-08-836-075A-107	Sequence 107, App	486	3	50.0	19	4	US-08-467-344A-432	Sequence 432, App
414	3	50.0	11	3	US-08-836-075A-108	Sequence 108, App	487	3	50.0	19	4	US-09-097-055B-45	Sequence 45, Appl
415	3	50.0	11	3	US-08-836-075A-109	Sequence 109, App	488	3	50.0	19	4	US-09-097-055B-51	Sequence 51, Appl
416	3	50.0	11	3	US-08-836-075A-110	Sequence 110, App	489	3	50.0	19	4	US-09-829-855-232	Sequence 232, App
417	3	50.0	11	3	US-08-836-075A-117	Sequence 117, App	490	3	50.0	20	1	US-08-382-013A-38	Sequence 38, Appl
418	3	50.0	11	4	US-09-142-680-16	Sequence 16, Appl	491	3	50.0	20	1	US-08-241-054-88	Sequence 88, Appl
419	3	50.0	11	4	US-09-430-503-15	Sequence 15, Appl	492	3	50.0	20	1	US-08-390-156A-74	Sequence 74, Appl
420	3	50.0	12	2	US-08-146-028-26	Sequence 26, Appl	493	3	50.0	20	1	US-08-419-009-4	Sequence 4, Appli
421	3	50.0	12	3	US-08-603-024-9	Sequence 9, Appli	494	3	50.0	20	1	US-08-439-817-68	Sequence 68, Appl
422	3	50.0	12	3	US-08-723-425A-26	Sequence 26, Appl	495	3	50.0	20	1	US-08-485-508-88	Sequence 88, Appl
423	3	50.0	12	3	US-09-112-206-26	Sequence 26, Appl	496	3	50.0	20	2	US-08-484-530-26	Sequence 26, Appl
424	3	50.0	12	4	US-09-407-687-24	Sequence 24, Appl	497	3	50.0	20	2	US-08-827-618A-26	Sequence 26, Appl
425	3	50.0	12	4	US-09-051-380-8	Sequence 8, Appli	498	3	50.0	20	3	US-08-483-952A-26	Sequence 26, Appl
426	3	50.0	12	4	US-09-403-752A-93	Sequence 93, Appl	499	3	50.0	20	3	US-08-894-017-27	Sequence 27, Appl
427	3	50.0	12	4	US-09-576-824A-26	Sequence 26, Appl	500	3	50.0	20	4	US-08-464-496-1	Sequence 1, Appli
428	3	50.0	13	2	US-08-480-190-26	Sequence 26, Appl	501	3	50.0	20	4	US-08-476-501-26	Sequence 26, Appl
429	3	50.0	13	2	US-08-488-379-26	Sequence 26, Appl	502	3	50.0	20	4	US-09-161-939A-1	Sequence 1, Appli
430	3	50.0	13	2	US-08-727-688-20	Sequence 20, Appl	503	3	50.0	20	4	US-09-161-939A-9	Sequence 9, Appli
431	3	50.0	13	3	US-08-727-308-8	Sequence 8, Appli	504	3	50.0	20	4	US-09-456-474-27	Sequence 27, Appl
432	3	50.0	13	4	US-08-475-399A-26	Sequence 26, Appl	505	3	50.0	20	4	PCT-US92-07218-1	Sequence 1, Appli
433	3	50.0	13	5	PCT-US93-07545-26	Sequence 26, Appl	506	3	50.0	20	5	US-08-612-840A-3	Sequence 3, Appli
434	3	50.0	14	2	US-08-480-190-176	Sequence 176, App	507	3	50.0	21	2	US-09-508-803-3	Sequence 3, Appli
435	3	50.0	14	2	US-08-488-379-176	Sequence 176, App	508	3	50.0	21	4	US-07-933-469A-6	Sequence 6, Appli
436	3	50.0	14	3	US-08-782-997A-7	Sequence 7, Appli	509	3	50.0	22	1	US-08-250-310-6	Sequence 6, Appli
437	3	50.0	14	3	US-08-682-791B-2	Sequence 2, Appli	510	3	50.0	22	1	US-08-439-404-6	Sequence 6, Appli
438	3	50.0	14	4	US-08-218-369-6	Sequence 6, Appli	511	3	50.0	22	1	US-08-839-327-6	Sequence 6, Appli
439	3	50.0	14	4	US-09-413-611A-2	Sequence 2, Appli	512	3	50.0	22	3	US-09-340-781B-6	Sequence 6, Appli
440	3	50.0	14	4	US-08-475-399A-176	Sequence 176, App	513	3	50.0	22	3	US-09-205-258-884	Sequence 884, App
441	3	50.0	14	5	PCT-US93-07545-176	Sequence 176, App	514	3	50.0	22	4	US-08-905-223-385	Sequence 385, App
442	3	50.0	14	5	PCT-US95-03742-6	Sequence 6, Appli	515	3	50.0	23	3	US-08-951-034B-7	Sequence 7, Appli
443	3	50.0	15	1	US-08-551-128A-1	Sequence 1, Appli	516	3	50.0	23	4	US-08-895-474-12	Sequence 12, Appl
444	3	50.0	15	4	US-09-829-855-223	Sequence 223, App	517	3	50.0	24	3	US-08-905-054B-23	Sequence 23, Appl
445	3	50.0	15	5	PCT-US93-06751-5	Sequence 5, Appli	518	3	50.0	24	4	US-09-721-108-248	Sequence 248, App
446	3	50.0	15	5	PCT-US93-06751-37	Sequence 37, Appl	519	3	50.0	24	4	US-09-721-108-249	Sequence 249, App
447	3	50.0	16	1	US-08-321-625-53	Sequence 53, Appl	520	3	50.0	24	4	US-09-721-108-250	Sequence 250, App
448	3	50.0	16	1	US-08-321-625-80	Sequence 80, Appl	521	3	50.0	24	4	PCT-US92-07813-23	Sequence 23, Appl
449	3	50.0	16	3	US-09-181-083-53	Sequence 53, Appl	522	3	50.0	24	5	US-08-480-190-155	Sequence 155, App
450	3	50.0	16	3	US-09-181-083-80	Sequence 80, Appl	523	3	50.0	25	2	US-08-488-379-155	Sequence 155, App
451	3	50.0	16	4	US-09-330-914A-11	Sequence 11, Appl	524	3	50.0	25	2	US-08-997-080-17	Sequence 17, Appl
452	3	50.0	16	4	US-09-073-009-66	Sequence 66, Appl	525	3	50.0	25	2	US-08-997-362-17	Sequence 17, Appl
453	3	50.0	16	4	US-09-073-010-66	Sequence 66, Appl	526	3	50.0	25	2	US-08-873-970-17	Sequence 17, Appl
454	3	50.0	16	4	US-09-750-754-53	Sequence 53, Appl	527	3	50.0	25	3	US-08-948-378A-18	Sequence 18, Appl
455	3	50.0	16	4	US-09-750-754-80	Sequence 80, Appl	528	3	50.0	25	3	US-09-095-855-17	Sequence 17, Appl
456	3	50.0	17	4	US-09-025-769B-223	Sequence 223, App	529	3	50.0	25	3	US-09-095-855-17	Sequence 17, Appl
457	3	50.0	18	1	US-08-487-568-41	Sequence 41, Appl	530	3	50.0	25	3	US-09-169-425C-18	Sequence 18, Appl
458	3	50.0	18	3	US-08-336-553A-53	Sequence 53, Appl	531	3	50.0	25	3	US-08-705-347A-17	Sequence 17, Appl
459	3	50.0	18	3	US-08-336-553A-54	Sequence 54, Appl	532	3	50.0	25	4	US-09-324-542-17	Sequence 17, Appl
460	3	50.0	18	3	US-08-909-954-12	Sequence 12, Appl	533	3	50.0	25	4	US-09-302-329A-4	Sequence 4, Appli
461	3	50.0	18	4	US-08-439-157-53	Sequence 53, Appl	534	3	50.0	25	4	US-09-205-426-17	Sequence 17, Appl
462	3	50.0	18	4	US-08-439-157-54	Sequence 54, Appl	535	3	50.0	25	4	US-09-200-643-17	Sequence 17, Appl
463	3	50.0	18	4	US-09-437-895-53	Sequence 53, Appl	536	3	50.0	25	4	US-09-440-344-1	Sequence 1, Appli
464	3	50.0	18	4	US-09-437-895-54	Sequence 54, Appl	537	3	50.0	25	4	US-08-475-399A-155	Sequence 155, App
465	3	50.0	18	4	US-09-407-687-36	Sequence 36, Appl	538	3	50.0	25	4	US-09-692-064-3	Sequence 3, Appli

539	3	50.0	25	4	US-09-552-802B-43	Sequence 43, Appl	612	3	50.0	36	4	US-09-515-965A-1212	Sequence 1212, Ap
540	3	50.0	25	4	US-09-759-960-18	Sequence 18, Appl	613	3	50.0	36	4	US-09-350-641C-1051	Sequence 1051, Ap
541	3	50.0	25	4	US-09-084-303B-296	Sequence 296, App	614	3	50.0	36	4	US-09-350-641C-1212	Sequence 1212, Ap
542	3	50.0	25	4	US-09-667-319-4	Sequence 4, Appli	615	3	50.0	37	1	US-08-118-270-212	Sequence 212, App
543	3	50.0	25	5	PCT-US93-07545-155	Sequence 155, App	616	3	50.0	37	1	US-07-929-206-5	Sequence 5, Appli
544	3	50.0	26	4	US-08-525-539A-21	Sequence 21, Appl	617	3	50.0	37	1	US-07-929-206-6	Sequence 6, Appli
545	3	50.0	26	4	US-09-152-060-117	Sequence 117, App	618	3	50.0	37	1	US-07-929-206-8	Sequence 8, Appli
546	3	50.0	26	4	US-08-469-260A-191	Sequence 191, App	619	3	50.0	37	1	US-08-682-485A-14	Sequence 14, Appl
547	3	50.0	26	4	US-09-407-687-39	Sequence 39, Appl	620	3	50.0	37	1	US-08-682-485A-16	Sequence 16, Appl
548	3	50.0	26	4	US-08-488-446-191	Sequence 191, App	621	3	50.0	37	1	US-08-682-485A-17	Sequence 17, Appl
549	3	50.0	26	4	US-08-467-344A-191	Sequence 191, App	622	3	50.0	37	1	US-08-682-485A-18	Sequence 18, Appl
550	3	50.0	27	2	US-08-967-999-8	Sequence 8, Appli	623	3	50.0	37	2	US-08-313-185-2	Sequence 2, Appli
551	3	50.0	27	2	US-08-967-999-9	Sequence 9, Appli	624	3	50.0	37	2	US-08-313-185-3	Sequence 3, Appli
552	3	50.0	27	3	US-08-256-747C-46	Sequence 46, Appl	625	3	50.0	37	2	US-08-459-499-5	Sequence 5, Appli
553	3	50.0	27	3	US-08-834-130A-46	Sequence 46, Appl	626	3	50.0	37	2	US-08-459-499-6	Sequence 6, Appli
554	3	50.0	28	1	US-08-402-282-5	Sequence 5, Appli	627	3	50.0	37	2	US-08-933-314-14	Sequence 14, Appl
555	3	50.0	28	1	US-08-508-004-5	Sequence 5, Appli	628	3	50.0	37	2	US-08-933-314-16	Sequence 16, Appl
556	3	50.0	28	1	US-08-402-066-5	Sequence 5, Appli	629	3	50.0	37	2	US-08-933-314-17	Sequence 17, Appl
557	3	50.0	28	1	US-08-402-068-5	Sequence 5, Appli	630	3	50.0	37	2	US-08-933-314-18	Sequence 18, Appl
558	3	50.0	28	4	US-09-407-687-38	Sequence 38, Appl	631	3	50.0	37	3	US-09-082-614A-2	Sequence 2, Appli
559	3	50.0	28	4	US-09-528-200-73	Sequence 73, Appl	632	3	50.0	37	3	US-09-082-614A-3	Sequence 3, Appli
560	3	50.0	29	3	US-08-895-474-11	Sequence 11, Appl	633	3	50.0	37	4	US-09-461-325-242	Sequence 242, App
561	3	50.0	29	4	US-09-058-740-3	Sequence 3, Appli	634	3	50.0	37	4	US-09-461-325-429	Sequence 429, App
562	3	50.0	29	4	US-09-205-258-630	Sequence 630, App	635	3	50.0	37	4	US-10-012-542-242	Sequence 242, App
563	3	50.0	29	4	US-09-690-454-161	Sequence 161, App	636	3	50.0	37	4	US-10-012-542-429	Sequence 429, App
564	3	50.0	30	1	US-08-117-083-25	Sequence 25, Appl	637	3	50.0	37	5	PCT-US93-08528-212	Sequence 212, App
565	3	50.0	31	1	US-08-055-917-1	Sequence 1, Appli	638	3	50.0	37	6	5177308-12	Patent No. 5177308
566	3	50.0	31	1	US-07-614-443A-6	Sequence 6, Appli	639	3	50.0	38	1	US-08-117-080-7	Sequence 7, Appli
567	3	50.0	31	1	US-08-095-068-1	Sequence 1, Appli	640	3	50.0	38	1	US-08-117-080-8	Sequence 8, Appli
568	3	50.0	31	1	US-07-934-656A-15	Sequence 15, Appl	641	3	50.0	38	1	US-08-176-500-134	Sequence 134, App
569	3	50.0	31	1	US-08-294-859-6	Sequence 6, Appli	642	3	50.0	38	1	US-08-118-270-210	Sequence 210, App
570	3	50.0	31	1	US-08-481-676-6	Sequence 6, Appli	643	3	50.0	38	1	US-08-118-270-211	Sequence 211, App
571	3	50.0	31	2	US-07-785-565A-1	Sequence 1, Appli	644	3	50.0	38	1	US-08-118-270-213	Sequence 213, App
572	3	50.0	32	1	US-08-140-721A-1	Sequence 1, Appli	645	3	50.0	38	1	US-08-471-052A-134	Sequence 134, App
573	3	50.0	32	1	US-08-619-790C-1	Sequence 1, Appli	646	3	50.0	38	1	US-08-471-329-7	Sequence 7, Appli
574	3	50.0	32	3	US-09-053-197A-68	Sequence 68, Appl	647	3	50.0	38	1	US-08-471-329-8	Sequence 8, Appli
575	3	50.0	32	4	US-09-085-761A-73	Sequence 73, Appl	648	3	50.0	38	1	US-08-189-331-134	Sequence 134, App
576	3	50.0	32	4	US-09-625-972-27	Sequence 27, Appl	649	3	50.0	38	1	US-08-682-485A-15	Sequence 15, Appl
577	3	50.0	32	4	US-09-308-345A-36	Sequence 36, Appl	650	3	50.0	38	1	US-08-682-485A-20	Sequence 20, Appl
578	3	50.0	32	4	US-09-308-345A-37	Sequence 37, Appl	651	3	50.0	38	2	US-08-471-939-134	Sequence 134, App
579	3	50.0	32	4	US-09-308-345A-39	Sequence 39, Appl	652	3	50.0	38	2	US-08-471-800-134	Sequence 134, App
580	3	50.0	32	4	US-09-308-345A-40	Sequence 40, Appl	653	3	50.0	38	2	US-08-915-142-7	Sequence 7, Appli
581	3	50.0	32	4	US-09-308-345A-41	Sequence 41, Appl	654	3	50.0	38	2	US-08-915-142-8	Sequence 8, Appli
582	3	50.0	33	1	US-08-290-448A-5	Sequence 5, Appli	655	3	50.0	38	2	US-08-471-068-134	Sequence 134, App
583	3	50.0	33	1	US-08-290-448A-6	Sequence 6, Appli	656	3	50.0	38	2	US-08-933-314-15	Sequence 15, Appl
584	3	50.0	33	1	US-08-290-448A-5	Sequence 5, Appli	657	3	50.0	38	2	US-08-933-314-20	Sequence 20, Appl
585	3	50.0	33	1	US-08-290-448A-6	Sequence 6, Appli	658	3	50.0	38	3	US-08-948-378A-6	Sequence 6, Appli
586	3	50.0	33	1	US-08-175-069A-5	Sequence 5, Appli	659	3	50.0	38	3	US-08-348-518C-21	Sequence 21, Appl
587	3	50.0	33	1	US-08-175-069A-6	Sequence 6, Appli	660	3	50.0	38	3	US-08-476-509B-21	Sequence 21, Appl
588	3	50.0	33	3	US-09-082-279B-1213	Sequence 1213, Ap	661	3	50.0	38	3	US-09-169-425C-6	Sequence 6, Appli
589	3	50.0	33	4	US-08-461-939B-5	Sequence 5, Appli	662	3	50.0	38	4	US-09-759-960-6	Sequence 6, Appli
590	3	50.0	33	4	US-08-461-939B-6	Sequence 6, Appli	663	3	50.0	38	4	US-09-646-691B-70	Sequence 70, Appl
591	3	50.0	33	4	US-08-464-000-5	Sequence 5, Appli	664	3	50.0	38	4	PCT-US93-08528-210	Sequence 210, App
592	3	50.0	33	4	US-08-464-000-6	Sequence 6, Appli	665	3	50.0	38	5	PCT-US93-08528-211	Sequence 211, App
593	3	50.0	33	4	US-09-315-304B-1213	Sequence 1213, Ap	666	3	50.0	38	5	PCT-US93-08528-213	Sequence 213, App
594	3	50.0	33	4	US-09-834-784-1213	Sequence 1213, Ap	667	3	50.0	38	6	5177308-8	Patent No. 5177308
595	3	50.0	33	4	US-09-515-965A-1213	Sequence 1213, Ap	668	3	50.0	39	1	US-08-118-270-214	Sequence 214, App
596	3	50.0	33	4	US-09-350-641C-1213	Sequence 1213, Ap	669	3	50.0	39	5	PCT-US93-08528-214	Sequence 214, App
597	3	50.0	35	1	US-08-190-802A-255	Sequence 255, App	670	3	50.0	40	3	US-08-803-346-65	Sequence 65, Appl
598	3	50.0	35	3	US-08-477-346-255	Sequence 255, App	671	3	50.0	40	3	US-08-988-856B-13	Sequence 13, Appl
599	3	50.0	35	4	US-08-473-089-255	Sequence 255, App	672	3	50.0	40	4	US-08-469-260A-541	Sequence 541, App
600	3	50.0	35	4	US-08-487-072A-255	Sequence 255, App	673	3	50.0	40	4	US-08-475-399A-275	Sequence 275, App
601	3	50.0	36	1	US-08-303-651-1	Sequence 1, Appli	674	3	50.0	40	4	US-08-488-446-541	Sequence 541, App
602	3	50.0	36	3	US-09-082-279B-1051	Sequence 1051, Ap	675	3	50.0	40	4	US-08-467-344A-541	Sequence 541, App
603	3	50.0	36	3	US-09-082-279B-1212	Sequence 1212, Ap	676	3	50.0	40	4	US-08-843-845-13	Sequence 13, Appl
604	3	50.0	36	4	US-09-315-304B-1051	Sequence 1051, Ap	677	3	50.0	40	5	PCT-US95-04910-10	Sequence 10, Appl
605	3	50.0	36	4	US-09-315-304B-1212	Sequence 1212, Ap	678	3	50.0	40	6	5196194-8	Patent No. 5196194
606	3	50.0	36	4	US-09-276-600-7	Sequence 7, Appli	679	3	50.0	41	2	US-08-117-952-793	Sequence 793, App
607	3	50.0	36	4	US-09-834-784-1051	Sequence 1051, Ap	680	3	50.0	41	3	US-09-172-841-17	Sequence 17, Appl
608	3	50.0	36	4	US-09-834-784-1212	Sequence 1212, Ap	681	3	50.0	41	4	US-09-227-357-618	Sequence 618, App
609	3	50.0	36	4	US-09-779-451-53	Sequence 53, Appl	682	3	50.0	41	4	US-08-951-621-17	Sequence 17, Appl
610	3	50.0	36	4	US-09-779-451-71	Sequence 71, Appl	683	3	50.0	41	6	5512648-1	Patent No. 5512648
611	3	50.0	36	4	US-09-515-965A-1051	Sequence 1051, Ap	684	3	50.0	42	2	US-08-488-161-79	Sequence 79, Appl

685	3	50.0	42	3	US-09-273-685-79	Sequence 79, Appl	758	3	50.0	54	4	US-09-730-763-19	Sequence 19, Appl
686	3	50.0	42	3	US-08-894-699-66	Sequence 66, Appl	759	3	50.0	54	4	US-09-429-370-12	Sequence 12, Appl
687	3	50.0	42	3	US-09-444-410-66	Sequence 66, Appl	760	3	50.0	54	4	US-09-429-370-15	Sequence 15, Appl
688	3	50.0	42	4	US-09-205-258-1013	Sequence 1013, Ap	761	3	50.0	54	4	US-09-429-370-16	Sequence 16, Appl
689	3	50.0	42	5	PCT-US95-11934-79	Sequence 79, Appl	762	3	50.0	54	4	US-09-429-370-19	Sequence 19, Appl
690	3	50.0	43	2	US-08-488-161-77	Sequence 77, Appl	763	3	50.0	54	4	US-09-402-181B-302	Sequence 302, App
691	3	50.0	43	3	US-09-273-685-77	Sequence 77, Appl	764	3	50.0	54	4	US-09-721-456-302	Sequence 302, App
692	3	50.0	43	3	US-08-988-856B-5	Sequence 5, Appli	765	3	50.0	54	4	US-09-621-976-4731	Sequence 4731, Ap
693	3	50.0	43	4	US-09-843-845-5	Sequence 5, Appli	766	3	50.0	55	1	US-08-366-953A-36	Sequence 36, Appl
694	3	50.0	43	5	PCT-US95-11934-77	Sequence 77, Appl	767	3	50.0	55	1	US-08-366-953A-37	Sequence 37, Appl
695	3	50.0	44	3	US-08-894-483-5	Sequence 5, Appli	768	3	50.0	55	1	US-08-366-953A-38	Sequence 38, Appl
696	3	50.0	46	4	US-09-779-451-51	Sequence 51, Appl	769	3	50.0	55	1	US-08-366-953A-39	Sequence 39, Appl
697	3	50.0	46	4	US-09-779-451-69	Sequence 69, Appl	770	3	50.0	55	1	US-08-366-953A-42	Sequence 42, Appl
698	3	50.0	48	1	US-08-290-448A-4	Sequence 4, Appli	771	3	50.0	55	1	US-08-366-953A-43	Sequence 43, Appl
699	3	50.0	48	1	US-08-290-448A-7	Sequence 7, Appli	772	3	50.0	55	1	US-08-366-953A-44	Sequence 44, Appl
700	3	50.0	48	1	US-08-290-448A-4	Sequence 4, Appli	773	3	50.0	55	4	US-09-621-976-4235	Sequence 4235, Ap
701	3	50.0	48	1	US-08-290-448A-7	Sequence 7, Appli	774	3	50.0	55	4	US-09-621-976-6267	Sequence 6267, Ap
702	3	50.0	48	1	US-08-175-069A-4	Sequence 4, Appli	775	3	50.0	55	4	US-09-621-976-7689	Sequence 7689, Ap
703	3	50.0	48	1	US-08-175-069A-7	Sequence 7, Appli	776	3	50.0	56	2	US-08-557-309B-28	Sequence 28, Appl
704	3	50.0	48	2	US-08-637-759B-199	Sequence 199, App	777	3	50.0	56	2	US-08-850-910A-24	Sequence 24, Appl
705	3	50.0	48	3	US-08-871-355A-199	Sequence 199, App	778	3	50.0	56	3	US-08-834-306-28	Sequence 28, Appl
706	3	50.0	48	4	US-08-461-939B-4	Sequence 4, Appli	779	3	50.0	56	3	US-08-993-674A-28	Sequence 28, Appl
707	3	50.0	48	4	US-08-461-939B-7	Sequence 7, Appli	780	3	50.0	56	4	US-09-227-357-671	Sequence 671, App
708	3	50.0	48	4	US-08-464-000-4	Sequence 4, Appli	781	3	50.0	56	4	US-08-894-626-4	Sequence 4, Appli
709	3	50.0	48	4	US-08-464-000-7	Sequence 7, Appli	782	3	50.0	56	4	US-09-256-976-28	Sequence 28, Appl
710	3	50.0	48	4	US-09-201-945-199	Sequence 199, App	783	3	50.0	56	4	US-09-205-258-359	Sequence 359, App
711	3	50.0	48	4	US-09-227-357-241	Sequence 241, App	784	3	50.0	56	4	US-09-621-976-6726	Sequence 6726, Ap
712	3	50.0	49	1	US-08-387-156-4	Sequence 4, Appli	785	3	50.0	57	4	US-09-621-976-6039	Sequence 6039, Ap
713	3	50.0	49	2	US-08-694-865-4	Sequence 4, Appli	786	3	50.0	57	4	US-09-621-976-6935	Sequence 6935, Ap
714	3	50.0	49	2	US-08-878-748-4	Sequence 4, Appli	787	3	50.0	58	2	US-08-408-095-34	Sequence 34, Appl
715	3	50.0	49	3	US-09-124-491-4	Sequence 4, Appli	788	3	50.0	58	3	US-09-369-494-1	Sequence 1, Appli
716	3	50.0	49	4	US-08-475-399A-276	Sequence 276, App	789	3	50.0	58	3	US-08-965-762-11	Sequence 11, Appl
717	3	50.0	49	4	US-09-383-912-4	Sequence 4, Appli	790	3	50.0	58	4	US-09-227-357-240	Sequence 240, App
718	3	50.0	49	4	US-09-148-545-245	Sequence 245, App	791	3	50.0	59	1	US-08-358-160-118	Sequence 118, App
719	3	50.0	50	1	US-07-614-443A-5	Sequence 5, Appli	792	3	50.0	59	3	US-08-513-974B-25	Sequence 25, Appl
720	3	50.0	50	1	US-08-294-859-5	Sequence 5, Appli	793	3	50.0	59	3	US-08-776-971-20	Sequence 20, Appl
721	3	50.0	50	1	US-08-481-676-5	Sequence 5, Appli	794	3	50.0	59	4	US-09-911-927-11	Sequence 11, Appl
722	3	50.0	50	3	US-09-053-197A-67	Sequence 67, Appl	795	3	50.0	59	4	US-09-911-882-11	Sequence 11, Appl
723	3	50.0	50	3	US-09-177-249-94	Sequence 94, Appl	796	3	50.0	59	4	US-09-638-715-33	Sequence 33, Appl
724	3	50.0	50	4	US-09-085-761A-72	Sequence 72, Appl	797	3	50.0	59	4	US-09-911-888-11	Sequence 11, Appl
725	3	50.0	51	2	US-08-464-517-13	Sequence 13, Appl	798	3	50.0	59	4	US-09-461-436B-25	Sequence 25, Appl
726	3	50.0	51	2	US-08-633-879C-10	Sequence 10, Appl	799	3	50.0	59	4	US-10-060-509-33	Sequence 33, Appl
727	3	50.0	51	2	US-08-246-361A-13	Sequence 13, Appl	800	3	50.0	59	4	US-09-621-976-4644	Sequence 4644, Ap
728	3	50.0	51	3	US-08-463-772-13	Sequence 13, Appl	801	3	50.0	59	4	US-09-621-976-5501	Sequence 5501, Ap
729	3	50.0	51	3	US-09-369-494-9	Sequence 9, Appli	802	3	50.0	59	4	US-10-060-506-33	Sequence 33, Appl
730	3	50.0	51	4	US-09-621-976-4432	Sequence 4432, Ap	803	3	50.0	59	6	5466783-13	Patent No. 5466783
731	3	50.0	51	4	US-09-621-976-4433	Sequence 4433, Ap	804	3	50.0	60	2	US-08-484-397A-28	Sequence 28, Appl
732	3	50.0	51	4	US-09-621-976-7188	Sequence 7188, Ap	805	3	50.0	60	2	US-08-484-397A-29	Sequence 29, Appl
733	3	50.0	51	4	US-09-621-976-7656	Sequence 7656, Ap	806	3	50.0	60	2	US-08-484-397A-30	Sequence 30, Appl
734	3	50.0	51	4	US-09-621-976-7660	Sequence 7660, Ap	807	3	50.0	60	2	US-08-484-397A-31	Sequence 31, Appl
735	3	50.0	51	5	PCT-US93-05000-13	Sequence 13, Appl	808	3	50.0	60	2	US-08-484-397A-34	Sequence 34, Appl
736	3	50.0	51	6	5274075-11	Sequence 13, Appl	809	3	50.0	60	2	US-08-484-397A-35	Sequence 35, Appl
737	3	50.0	52	3	US-09-165-042-6	Sequence 6, Appli	810	3	50.0	60	2	US-08-484-397A-36	Sequence 36, Appl
738	3	50.0	52	3	US-09-369-494-17	Sequence 17, Appl	811	3	50.0	60	2	US-08-484-397A-37	Sequence 37, Appl
739	3	50.0	52	3	US-09-358-569D-15	Sequence 15, Appl	812	3	50.0	60	4	US-09-638-715-20	Sequence 20, Appl
740	3	50.0	52	4	US-09-621-976-5773	Sequence 5773, Ap	813	3	50.0	60	4	US-09-638-715-21	Sequence 21, Appl
741	3	50.0	52	4	US-09-621-976-7672	Sequence 7672, Ap	814	3	50.0	60	4	US-09-205-258-407	Sequence 407, App
742	3	50.0	54	3	US-08-917-299-12	Sequence 12, Appl	815	3	50.0	60	4	US-10-060-509-20	Sequence 20, Appl
743	3	50.0	54	3	US-08-917-299-15	Sequence 15, Appl	816	3	50.0	60	4	US-10-060-509-21	Sequence 21, Appl
744	3	50.0	54	3	US-08-917-299-16	Sequence 16, Appl	817	3	50.0	60	4	US-09-663-600A-113	Sequence 113, App
745	3	50.0	54	3	US-08-917-299-19	Sequence 19, Appl	818	3	50.0	60	4	US-09-107-532A-7289	Sequence 7289, Ap
746	3	50.0	54	3	US-08-851-843A-183	Sequence 183, App	819	3	50.0	60	4	US-09-489-039A-8043	Sequence 8043, Ap
747	3	50.0	54	3	US-08-974-549A-302	Sequence 302, App	820	3	50.0	60	4	US-10-060-506-20	Sequence 20, Appl
748	3	50.0	54	3	US-09-422-662-12	Sequence 12, Appl	821	3	50.0	60	4	US-10-060-506-21	Sequence 21, Appl
749	3	50.0	54	3	US-09-422-662-15	Sequence 15, Appl	822	3	50.0	61	4	US-09-149-476-380	Sequence 380, App
750	3	50.0	54	3	US-09-422-662-16	Sequence 16, Appl	823	3	50.0	61	4	US-09-106-568E-148	Sequence 148, App
751	3	50.0	54	3	US-09-422-662-19	Sequence 19, Appl	824	3	50.0	61	4	US-09-345-236B-116	Sequence 116, App
752	3	50.0	54	3	US-08-854-050-183	Sequence 183, App	825	3	50.0	61	4	US-09-205-258-260	Sequence 260, App
753	3	50.0	54	4	US-09-430-323-183	Sequence 183, App	826	3	50.0	61	4	US-09-205-258-478	Sequence 478, App
754	3	50.0	54	4	US-09-205-258-767	Sequence 767, App	827	3	50.0	61	4	US-09-107-532A-5825	Sequence 5825, Ap
755	3	50.0	54	4	US-09-730-763-12	Sequence 12, Appl	828	3	50.0	61	4	US-09-489-039A-12622	Sequence 12622, A
756	3	50.0	54	4	US-09-730-763-15	Sequence 15, Appl	829	3	50.0	61	4	US-09-621-976-5989	Sequence 5989, Ap
757	3	50.0	54	4	US-09-730-763-16	Sequence 16, Appl	830	3	50.0	62	3	US-08-894-483-8	Sequence 8, Appli

831	3	50.0	62	4	US-09-252-991A-28943	Sequence 28943, A	904	3	50.0	73	4	US-09-134-000C-4681	Sequence 4681, Ap
832	3	50.0	62	4	US-09-543-681A-7871	Sequence 7871, Ap	905	3	50.0	73	4	US-09-621-976-6092	Sequence 6092, Ap
833	3	50.0	63	4	US-09-252-991A-23832	Sequence 23832, A	906	3	50.0	74	1	US-08-379-538-3	Sequence 3, Appli
834	3	50.0	63	4	US-08-311-731A-311	Sequence 311, App	907	3	50.0	74	1	US-08-379-538-4	Sequence 4, Appli
835	3	50.0	63	4	US-09-489-039A-7967	Sequence 7967, Ap	908	3	50.0	74	1	US-08-379-538-5	Sequence 5, Appli
836	3	50.0	64	4	US-09-632-287A-14	Sequence 14, Appl	909	3	50.0	74	4	US-09-252-991A-26625	Sequence 26625, A
837	3	50.0	64	4	US-09-134-000C-6722	Sequence 6722, Ap	910	3	50.0	74	4	US-09-252-991A-26626	Sequence 26626, A
838	3	50.0	64	4	US-09-673-395A-244	Sequence 244, App	911	3	50.0	74	4	US-09-252-991A-30664	Sequence 30664, A
839	3	50.0	64	4	US-09-188-930-297	Sequence 297, App	912	3	50.0	74	4	US-09-489-039A-12609	Sequence 12609, A
840	3	50.0	65	3	US-09-312-283C-297	Sequence 297, App	913	3	50.0	74	4	US-09-621-976-5521	Sequence 5521, Ap
841	3	50.0	65	4	US-09-543-681A-7660	Sequence 7660, Ap	914	3	50.0	74	4	US-09-621-976-5823	Sequence 5823, Ap
842	3	50.0	65	4	US-09-540-236-3382	Sequence 3382, Ap	915	3	50.0	75	3	US-08-803-346-60	Sequence 60, Appl
843	3	50.0	65	4	US-09-540-236-3543	Sequence 3543, Ap	916	3	50.0	75	3	US-08-803-346-61	Sequence 543, App
844	3	50.0	65	4	US-09-540-236-3543	Sequence 3543, Ap	917	3	50.0	75	4	US-09-149-476-543	Sequence 5558, Ap
845	3	50.0	66	4	US-09-134-001C-4484	Sequence 4484, Ap	918	3	50.0	75	4	US-09-328-352-5558	Sequence 11726, A
846	3	50.0	66	4	US-09-489-039A-13879	Sequence 13879, A	919	3	50.0	75	4	US-09-489-039A-11726	Sequence 19, Appl
847	3	50.0	66	4	US-09-540-236-3266	Sequence 3266, Ap	920	3	50.0	76	3	US-08-851-362D-19	Sequence 22, Appl
848	3	50.0	67	1	US-08-278-089A-27	Sequence 27, Appl	921	3	50.0	76	3	US-08-851-362D-22	Sequence 61, Appl
849	3	50.0	67	2	US-08-838-957A-26	Sequence 26, Appl	922	3	50.0	76	3	US-08-803-346-61	Sequence 30006, A
850	3	50.0	67	4	US-09-489-039A-12467	Sequence 12467, A	923	3	50.0	76	4	US-09-252-991A-30006	Sequence 281, App
851	3	50.0	67	4	US-09-621-976-6282	Sequence 6282, Ap	924	3	50.0	76	4	US-08-311-731A-281	Sequence 202, App
852	3	50.0	67	4	US-09-621-976-7214	Sequence 7214, Ap	925	3	50.0	76	4	US-09-084-303B-202	Sequence 5645, Ap
853	3	50.0	67	4	US-09-621-976-7215	Sequence 7215, Ap	926	3	50.0	76	4	US-09-621-976-5645	Sequence 85, Appl
854	3	50.0	68	3	US-08-513-974B-311	Sequence 311, App	927	3	50.0	76	4	US-09-472-087-85	Sequence 34, Appl
855	3	50.0	68	3	US-08-776-971-128	Sequence 128, App	928	3	50.0	77	3	US-08-888-429A-34	Sequence 29466, A
856	3	50.0	68	3	US-08-803-346-58	Sequence 58, Appl	929	3	50.0	77	4	US-09-252-991A-29466	Sequence 31687, A
857	3	50.0	68	4	US-09-252-991A-30574	Sequence 30574, A	930	3	50.0	77	4	US-09-593-653-34	Sequence 34, Appl
858	3	50.0	68	4	US-09-489-039A-9877	Sequence 9877, Ap	931	3	50.0	77	4	US-09-069-827A-118	Sequence 118, App
859	3	50.0	68	4	US-09-134-000C-3816	Sequence 3816, Ap	932	3	50.0	77	4	US-09-673-395A-288	Sequence 288, App
860	3	50.0	68	4	US-09-540-236-1990	Sequence 1990, Ap	933	3	50.0	77	4	US-09-621-976-4163	Sequence 4163, Ap
861	3	50.0	69	2	US-08-245-511-31	Sequence 31, Appl	934	3	50.0	77	4	US-09-621-976-5520	Sequence 5520, Ap
862	3	50.0	69	2	US-08-245-511-32	Sequence 32, Appl	935	3	50.0	77	4	US-08-612-788-22	Sequence 22, Appl
863	3	50.0	69	2	US-08-600-993A-31	Sequence 31, Appl	936	3	50.0	78	2	US-09-066-028-22	Sequence 22, Appl
864	3	50.0	69	2	US-08-600-993A-32	Sequence 32, Appl	937	3	50.0	78	3	US-08-469-260A-234	Sequence 234, App
865	3	50.0	69	3	US-08-905-223-353	Sequence 353, App	938	3	50.0	78	4	US-09-335-325-22	Sequence 22, Appl
866	3	50.0	69	4	US-09-252-991A-19264	Sequence 19264, A	939	3	50.0	78	4	US-09-716-865-20	Sequence 20, Appl
867	3	50.0	69	4	US-09-107-532A-6826	Sequence 6826, Ap	940	3	50.0	78	4	US-08-488-446-234	Sequence 234, App
868	3	50.0	69	4	US-09-489-039A-11833	Sequence 11833, A	941	3	50.0	78	4	US-09-328-352-6988	Sequence 6988, Ap
869	3	50.0	69	4	US-09-489-039A-12452	Sequence 12452, A	942	3	50.0	78	4	US-08-467-344A-234	Sequence 234, App
870	3	50.0	70	3	US-09-242-050-4	Sequence 4, Appli	943	3	50.0	78	4	US-09-540-236-2668	Sequence 2668, Ap
871	3	50.0	70	3	US-08-905-223-355	Sequence 355, App	944	3	50.0	79	4	US-09-345-236B-95	Sequence 95, Appl
872	3	50.0	70	3	US-08-905-223-469	Sequence 469, App	945	3	50.0	79	4	US-09-198-452A-1187	Sequence 1187, Ap
873	3	50.0	70	4	US-09-134-001C-5312	Sequence 5312, Ap	946	3	50.0	79	4	US-08-311-731A-270	Sequence 270, App
874	3	50.0	70	4	US-09-904-615-68	Sequence 68, Appl	947	3	50.0	79	4	US-09-107-532A-5914	Sequence 5914, Ap
875	3	50.0	70	4	US-09-148-545-143	Sequence 143, App	948	3	50.0	79	4	US-09-540-236-3183	Sequence 3183, Ap
876	3	50.0	70	4	US-09-673-395A-281	Sequence 281, App	949	3	50.0	79	4	US-09-252-991A-28197	Sequence 28197, A
877	3	50.0	70	4	US-09-621-976-5707	Sequence 5707, Ap	950	3	50.0	80	4	US-09-252-991A-31270	Sequence 31270, A
878	3	50.0	70	4	US-09-621-976-6084	Sequence 6084, Ap	951	3	50.0	80	4	US-08-311-731A-344	Sequence 344, App
879	3	50.0	71	1	US-08-055-917-15	Sequence 15, Appl	952	3	50.0	80	4	US-09-543-681A-7619	Sequence 7619, Ap
880	3	50.0	71	1	US-08-055-917-17	Sequence 17, Appl	953	3	50.0	80	4	US-08-858-207A-336	Sequence 336, App
881	3	50.0	71	1	US-08-095-068-15	Sequence 15, Appl	954	3	50.0	81	4	US-08-469-260A-187	Sequence 187, App
882	3	50.0	71	1	US-08-095-068-17	Sequence 17, Appl	955	3	50.0	81	4	US-08-220-602B-25	Sequence 25, Appl
883	3	50.0	71	1	US-08-140-721A-15	Sequence 15, Appl	956	3	50.0	81	4	US-08-488-446-187	Sequence 187, App
884	3	50.0	71	1	US-08-140-721A-17	Sequence 17, Appl	957	3	50.0	81	4	US-08-467-344A-187	Sequence 187, App
885	3	50.0	71	1	US-08-280-443-22	Sequence 22, Appl	958	3	50.0	81	4	US-09-489-039A-9095	Sequence 9095, Ap
886	3	50.0	71	1	US-08-457-459-22	Sequence 22, Appl	959	3	50.0	81	4	US-08-244-116B-21	Sequence 21, Appl
887	3	50.0	71	1	US-08-619-790C-15	Sequence 15, Appl	960	3	50.0	82	1	US-09-621-976-4787	Sequence 4787, Ap
888	3	50.0	71	1	US-08-619-790C-17	Sequence 17, Appl	961	3	50.0	82	4	US-09-621-976-6397	Sequence 6397, Ap
889	3	50.0	71	1	US-08-555-678-22	Sequence 22, Appl	962	3	50.0	82	4	US-08-889-291-12	Sequence 12, Appl
890	3	50.0	71	2	US-07-785-565A-15	Sequence 15, Appl	963	3	50.0	83	3	US-09-098-244-12	Sequence 12, Appl
891	3	50.0	71	2	US-07-785-565A-17	Sequence 17, Appl	964	3	50.0	83	4	US-09-690-454-51	Sequence 51, Appl
892	3	50.0	71	4	US-09-621-976-5666	Sequence 5666, Ap	965	3	50.0	83	4	US-09-543-681A-7622	Sequence 7622, Ap
893	3	50.0	71	4	US-09-621-976-5970	Sequence 5970, Ap	966	3	50.0	83	4	US-09-489-039A-7681	Sequence 7681, Ap
894	3	50.0	71	4	US-09-621-976-6815	Sequence 6815, Ap	967	3	50.0	83	4	US-09-489-039A-12154	Sequence 12154, A
895	3	50.0	71	5	PCT-US95-02275-22	Sequence 22, Appl	968	3	50.0	83	4	US-09-673-395A-279	Sequence 279, App
896	3	50.0	72	4	US-09-107-532A-6178	Sequence 6178, Ap	969	3	50.0	84	2	US-08-353-476-77	Sequence 77, Appl
897	3	50.0	72	4	US-09-489-039A-11635	Sequence 11635, A	970	3	50.0	84	2	US-08-353-476-78	Sequence 78, Appl
898	3	50.0	72	4	US-09-621-976-4838	Sequence 4838, Ap	971	3	50.0	84	4	US-08-679-493A-96	Sequence 96, Appl
899	3	50.0	73	1	US-08-379-538-7	Sequence 7, Appli	972	3	50.0	84	4		
900	3	50.0	73	3	US-08-483-533-32	Sequence 32, Appl	973	3	50.0	84	4		
901	3	50.0	73	3	US-08-483-533-34	Sequence 34, Appl	974	3	50.0	84	4		
902	3	50.0	73	4	US-09-283-471A-32	Sequence 32, Appl	975	3	50.0	84	4		
903	3	50.0	73	4	US-09-283-471A-34	Sequence 34, Appl	976	3	50.0	84	4		

977 3 50.0 84 4 US-08-679-493A-97 Sequence 97, Appl
978 3 50.0 84 4 US-09-818-236A-2 Sequence 2, Appli
979 3 50.0 84 4 US-09-540-236-1937 Sequence 1937, Ap
980 3 50.0 85 4 US-09-205-258-637 Sequence 637, App
981 3 50.0 85 4 US-09-252-991A-32597 Sequence 32597, A
982 3 50.0 85 4 US-09-938-806A-4 Sequence 4, Appli
983 3 50.0 85 4 US-09-698-286A-10 Sequence 10, Appl
984 3 50.0 86 3 US-08-905-223-280 Sequence 280, App
985 3 50.0 86 4 US-09-252-991A-32155 Sequence 32155, A
986 3 50.0 86 4 US-09-107-532A-7054 Sequence 7054, Ap
987 3 50.0 86 4 US-09-621-976-4094 Sequence 4094, Ap
988 3 50.0 86 4 US-09-621-976-7220 Sequence 7220, Ap
989 3 50.0 87 4 US-09-227-357-544 Sequence 544, App
990 3 50.0 88 3 US-09-216-295-17 Sequence 17, Appl
991 3 50.0 88 4 US-09-482-273-178 Sequence 178, App
992 3 50.0 88 4 US-09-482-273-179 Sequence 179, App
993 3 50.0 88 4 US-09-621-976-3972 Sequence 3972, Ap
994 3 50.0 88 4 US-09-621-976-5291 Sequence 5291, Ap
995 3 50.0 89 4 US-09-252-991A-18338 Sequence 18338, A
996 3 50.0 89 4 US-09-328-352-6573 Sequence 6573, Ap
997 3 50.0 89 4 US-09-543-681A-7216 Sequence 7216, Ap
998 3 50.0 89 4 US-09-489-039A-8463 Sequence 8463, Ap
999 3 50.0 89 4 US-09-621-976-6241 Sequence 6241, Ap
1000 3 50.0 89 4 US-09-621-976-7155 Sequence 7155, Ap

ALIGNMENTS

RESULT 1
US-09-252-991A-18367
; Sequence 18367, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18367
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367

Query Match 83.3%; Score 5; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
|||||

Db 2 DWSWA 6

RESULT 2
US-09-252-991A-31533
; Sequence 31533, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31533
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533

Query Match 83.3%; Score 5; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||||

Db 94 ADWSW 98

RESULT 3
US-09-325-932A-163
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163

Query Match 83.3%; Score 5; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||||

Db 109 ADWSW 113

RESULT 4
US-09-325-932A-162
; Sequence 162, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-162

Query Match 83.3%; Score 5; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||||

Db 100 ADWSW 104

RESULT 5

US-09-632-570-17

; Sequence 17, Application US/09632570

; Patent No. 6623949

; GENERAL INFORMATION:

; APPLICANT: Gualfetti, Peter

; APPLICANT: Mitchinson, Colin

; APPLICANT: Phillips, Jay Ian

; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase

; FILE REFERENCE: GC631

; CURRENT APPLICATION NUMBER: US/09/632,570

; CURRENT FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Gliocladium roseum (3)

US-09-632-570-17

Query Match 83.3%; Score 5; DB 4; Length 236;

Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 63 ADWSW 67

RESULT 6

US-09-632-575-47

; Sequence 47, Application US/09632575

; Patent No. 6635465

; GENERAL INFORMATION:

; APPLICANT: Gualfetti, Peter

; APPLICANT: Mitchinson, Colin

; APPLICANT: Ropp, Traci M.

; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding

; FILE REFERENCE: GC629

; CURRENT APPLICATION NUMBER: US/09/632,575

; CURRENT FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 47

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Gliocladium roseum (3)

US-09-632-575-47

Query Match 83.3%; Score 5; DB 4; Length 236;

Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 63 ADWSW 67

RESULT 7

US-09-345-236B-3

; Sequence 3, Application US/09345236B

; Patent No. 6521454

; GENERAL INFORMATION:

; APPLICANT: Becnel, James J.

; APPLICANT: Tuku, Fukuda

; APPLICANT: Moser, Bettina

; APPLICANT: Cockburn, Andrew

; APPLICANT: White, Susan E.

; APPLICANT: Undeen, Albert H.

; TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal

; FILE REFERENCE: 21042.0004

; CURRENT APPLICATION NUMBER: US/09/345,236B

; CURRENT FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 242

; TYPE: PRT

; ORGANISM: mosquito baculovirus

US-09-345-236B-3

Query Match 83.3%; Score 5; DB 4; Length 242;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6

Db 80 DWSWA 84

RESULT 8

US-09-325-932A-158

; Sequence 158, Application US/09325932A

; Patent No. 6451604

; GENERAL INFORMATION:

; APPLICANT: Flinn, Barry

; APPLICANT: Lasham, Annette

; TITLE OF INVENTION: Compositions affecting programmed cell

; TITLE OF INVENTION: death and their use in the modification of forestry plant develop

; FILE REFERENCE: 1022

; CURRENT APPLICATION NUMBER: US/09/325,932A

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 206

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 158

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

US-09-325-932A-158

Query Match 83.3%; Score 5; DB 4; Length 378;

Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 128 ADWSW 132

RESULT 9

US-09-252-991A-22368

; Sequence 22368, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 22368

; LENGTH: 445

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22368

Query Match 83.3%; Score 5; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
| | | | |
Db 304 DWSWA 308

RESULT 10
US-09-252-991A-21704
; Sequence 21704, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21704
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match 83.3%; Score 5; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
| | | | |
Db 169 DWSWA 173

RESULT 11
5217869-75
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:75:
; LENGTH: 5
5217869-75

Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
| | | | |
Db 1 DWSW 4

RESULT 12
US-08-435-925C-9
; Sequence 9, Application US/08435925C
; Patent No. 5646025
; GENERAL INFORMATION:
; APPLICANT: Moyer, Donna
; TITLE OF INVENTION: SCY TALIDUM CATALASE GENE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5646025o No. 5646025disk of No. 5646025th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,925C
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4429.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-925C-9

Query Match 66.7%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
| | | | |
Db 1 ADWS 4

RESULT 13
US-08-435-925C-10
; Sequence 10, Application US/08435925C
; Patent No. 5646025
; GENERAL INFORMATION:
; APPLICANT: Moyer, Donna
; TITLE OF INVENTION: SCY TALIDUM CATALASE GENE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5646025o No. 5646025disk of No. 5646025th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,925C
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4429.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
| | | | |
Db 1 DWSW 4

RESULT 12
US-08-435-925C-9
; Sequence 9, Application US/08435925C
; Patent No. 5646025
; GENERAL INFORMATION:
; APPLICANT: Moyer, Donna
; TITLE OF INVENTION: SCY TALIDUM CATALASE GENE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-925C-10

Query Match 66.7%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 1 ADWS 4

RESULT 14
US-08-190-788A-246
; Sequence 246, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-246

Query Match 66.7%; Score 4; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 7 ADWS 10

RESULT 15
US-08-383-474B-249
; Sequence 249, Application US/08383474B

; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-249

Query Match 66.7%; Score 4; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||
Db 7 ADWS 10

RESULT 16
US-08-465-391A-246
; Sequence 246, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331viel, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-246

Query Match 66.7%; Score 4; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|
|
|
|
Db 7 ADWS 10

RESULT 17
US-08-464-538B-246
Sequence 246, Application US/08464538B
Patent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillipe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-246

Query Match 66.7%; Score 4; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|
|
|
|
Db 7 ADWS 10

RESULT 18
US-08-463-076E-303
Sequence 303, Application US/08463076E
Patent No. 5880096
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 303:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid

us-09-847-940c-6.oligo.rai

Mon Jul 26 09:11:20 2004

```
; TELEPHONE: (212) 573-4585
; TELEFAX: (212) 573-1939
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Filistata hibernalis
; TISSUE TYPE: venom
US-08-379-538-2

Query Match 66.7%; Score 4; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
Db 52 DWSW 55

RESULT 22
US-09-177-249-184
; Sequence 184, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 184
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-184

Query Match 66.7%; Score 4; DB 3; Length 78;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 54 ADWS 57

RESULT 23
US-09-252-991A-27207
; Sequence 27207, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

```
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27207
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27207

Query Match 66.7%; Score 4; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 13 ADWS 16

RESULT 24
US-09-621-976-4160
; Sequence 4160, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4160
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -15...-1
; NAME/KEY: UNSURE
; LOCATION: 46
; OTHER INFORMATION: Xaa = Asn,Ser
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = Lys,Thr
US-09-621-976-4160

Query Match 66.7%; Score 4; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
Db 39 WSWA 42

RESULT 25
US-09-251-372-4
; Sequence 4, Application US/09251372
; Patent No. 6238886
; GENERAL INFORMATION:
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
```


;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/251,372
; FILING DATE: 16-FEB-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9900823.7
; FILING DATE: 14-JAN-1999
; APPLICATION NUMBER: 9803290.7
; FILING DATE: 16-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30012A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-251-372-4

Query Match 66.7%; Score 4; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
|||
Db 72 WSWA 75

RESULT 26
US-09-811-241-4
; Sequence 4, Application US/09811241
; Patent No. 6348341
; GENERAL INFORMATION:
; APPLICANT: PATEL, LISA
; APPLICANT: MACPHEE, COLIN HOUSTON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30012A-D1
; CURRENT APPLICATION NUMBER: US/09/811,241
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/251,372
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 9900823.7
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 9803290.7
; PRIOR FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 84
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-811-241-4

Query Match 66.7%; Score 4; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
|||
Db 72 WSWA 75

RESULT 27
US-09-252-991A-19040
; Sequence 19040, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19040
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19040

Query Match 66.7%; Score 4; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
|||
Db 32 ADWS 35

RESULT 28
US-09-252-991A-31932
; Sequence 31932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31932
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31932

Query Match 66.7%; Score 4; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
|||
Db 91 WSWA 94

RESULT 29
US-08-241-853-28
; Sequence 28, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37


```

; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-241-853-29
;
; Query Match 66.7%; Score 4; DB 1; Length 100;
; Best Local Similarity 100.0%; Pred. No. 47;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 DWSW 5
Db 20 DWSW 23
;
; RESULT 31
; US-08-850-917-28
; Sequence 28, Application US/08850917
; Patent No. 5854045
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,917
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,853
; FILING DATE: 12-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-850-917-28
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-241-853-29
;
; Query Match 66.7%; Score 4; DB 1; Length 100;
; Best Local Similarity 100.0%; Pred. No. 47;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 DWSW 5
Db 20 DWSW 23
;
; RESULT 30
; US-08-241-853-29
; Sequence 29, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-241-853-29
;
; Query Match 66.7%; Score 4; DB 1; Length 100;
; Best Local Similarity 100.0%; Pred. No. 47;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 DWSW 5
Db 20 DWSW 23
;
; RESULT 31
; US-08-850-917-28
; Sequence 28, Application US/08850917
; Patent No. 5854045
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,917
; FILING DATE: 02-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,853
; FILING DATE: 12-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-850-917-28
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-850-917-28
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-241-853-29
;
; Query Match 66.7%; Score 4; DB 1; Length 100;
; Best Local Similarity 100.0%; Pred. No. 47;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 DWSW 5
Db 20 DWSW 23
;
; RESULT 30
; US-08-241-853-29
; Sequence 29, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-241-853-29
;
; Query Match 66.7%; Score 4; DB 1; Length 100;
; Best Local Similarity 100.0%; Pred. No. 47;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 DWSW 5
Db 20 DWSW 23
;
; RESULT 31
; US-08-850-917-28
; Sequence 28, Application US/08850917
; Patent No. 5854045
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,917
; FILING DATE: 02
```


TELEFAX: (650)328-4477
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-788-621B-4

Query Match 66.7%; Score 4; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 52 ADWS 55

RESULT 37

US-08-477-270-20
Sequence 20, Application US/08477270
Patent No. 5629158
GENERAL INFORMATION:
APPLICANT: UHLEN, Mathias
TITLE OF INVENTION: SOLID PHASE DIAGNOSIS OF MEDICAL
CONDITIONS
TITLE OF INVENTION: CONDITIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,270
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/261,010
FILING DATE:
APPLICATION NUMBER: US 07/781,157
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16787/153 DFBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-270-20

Query Match 66.7%; Score 4; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 31 ADWS 34

RESULT 38
US-09-149-476-360
Sequence 360, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11

us-09-847-940c-6.oligo.rai

Mon Jul 26 09:11:20 2004

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 66.7%; Score 4; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
|||
Db 32 WSWA 35

RESULT 39
US-09-673-395A-204
; Sequence 204, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS

; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595


```
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-204

Query Match      66.7%; Score 4; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 WSWA 6
      ||||
Db      102 WSWA 105

RESULT 40
US-09-543-681A-7177
; Sequence 7177, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7177
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7177

Query Match      66.7%; Score 4; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
      ||||
Db      94 ADWS 97

RESULT 41
US-09-252-991A-20154
; Sequence 20154, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20154
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817

Query Match      66.7%; Score 4; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 WSWA 6
      ||||
Db      134 WSWA 137

RESULT 42
US-09-257-583-13
; Sequence 13, Application US/09257583A
; Patent No. 6429362
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/257,583A
; CURRENT FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-09-257-583-13

Query Match      66.7%; Score 4; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
      ||||
Db      45 ADWS 48

RESULT 43
US-09-252-991A-23817
; Sequence 23817, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23817
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817

Query Match      66.7%; Score 4; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 WSWA 6
      ||||
Db      134 WSWA 137

RESULT 44
US-09-199-637A-339
```

```
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20154

Query Match      66.7%; Score 4; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
      ||||
Db      45 ADWS 48

RESULT 42
US-09-257-583-13
; Sequence 13, Application US/09257583A
; Patent No. 6429362
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/257,583A
; CURRENT FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-09-257-583-13

Query Match      66.7%; Score 4; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
      ||||
Db      87 ADWS 90

RESULT 43
US-09-252-991A-23817
; Sequence 23817, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23817
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817

Query Match      66.7%; Score 4; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 WSWA 6
      ||||
Db      134 WSWA 137

RESULT 44
US-09-199-637A-339
```



```
; Sequence 339, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-339

Query Match      66.7%; Score 4; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 75;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSW 5
      |||||
Db      31 DWSW 34

RESULT 45
US-09-252-991A-23876
; Sequence 23876, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23876
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23876

Query Match      66.7%; Score 4; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 75;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
      |||||
Db      56 ADWS 59

RESULT 46
US-09-252-991A-17160
; Sequence 17160, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```

```
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17160
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17160

Query Match      66.7%; Score 4; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 82;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 WSWA 6
      |||||
Db      61 WSWA 64

RESULT 47
US-09-252-991A-28753
; Sequence 28753, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28753
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28753

Query Match      66.7%; Score 4; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 83;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
      |||||
Db      158 ADWS 161

RESULT 48
US-09-134-000C-3705
; Sequence 3705, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3705
; LENGTH: 191
; TYPE: PRT
```



```

; ORGANISM: Enterococcus faecalis
US-09-134-000C-3705

Query Match      66.7%; Score 4; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      162 ADWS 165

RESULT 49
US-09-489-039A-12525
; Sequence 12525, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12525
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12525

Query Match      66.7%; Score 4; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      147 ADWS 150

RESULT 50
US-09-540-236-2208
; Sequence 2208, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2208
; LENGTH: 201
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2208

Query Match      66.7%; Score 4; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      120 ADWS 123

Search completed: July 23, 2004, 13:28:17
Job time : 28 secs
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:20:30 ; Search time 52 Seconds
(without alignments)
32.602 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 6

Sequence: 1 ADWSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	5	AAM48538 Anti-infl
2	6	100.0	6	5	AAM48570 Anti-infl
3	6	100.0	6	6	ADA61814 NFkB esse
4	6	100.0	6	6	ADA61846 NFkB esse
5	6	100.0	7	5	AAM48574 Anti-infl
6	6	100.0	7	6	ADA61850 NFkB esse
7	6	100.0	8	5	AAM48575 Anti-infl
8	6	100.0	8	5	AAM48567 Anti-infl
9	6	100.0	8	6	ADA61851 NFkB esse
10	6	100.0	8	6	ADA61843 NFkB esse
11	6	100.0	9	5	AAM48573 Anti-infl
12	6	100.0	9	5	AAM48566 Anti-infl
13	6	100.0	9	5	AAM48569 Anti-infl
14	6	100.0	9	5	AAM48572 Anti-infl
15	6	100.0	9	6	ADA61848 NFkB esse
16	6	100.0	9	6	ADA61841 NFkB esse
17	6	100.0	9	6	ADA61849 NFkB esse
18	6	100.0	9	6	ADA61845 NFkB esse
19	6	100.0	9	6	ADA61842 NFkB esse
20	6	100.0	10	5	AAM48568 Anti-infl
21	6	100.0	10	5	AAM48571 Anti-infl
22	6	100.0	10	6	ADA61844 NFkB esse
23	6	100.0	10	6	ADA61847 NFkB esse
24	6	100.0	11	5	AAM48565 Anti-infl
25	6	100.0	11	6	ADA61840 NFkB esse

99	5	83.3	277	7	ADB94916	Adb94916	Programme	172	4	66.7	17	6	ADA61932	Ada61932	NfKb	esse
100	5	83.3	289	4	ABG24678	Abg24678	Novel hum	173	4	66.7	17	6	ADA61915	Ada61915	NfKb	esse
101	5	83.3	371	4	AAM41230	Aam41230	Human pol	174	4	66.7	17	6	ADA61914	Ada61914	NfKb	esse
102	5	83.3	378	4	AAB65775	Aab65775	Cysteine	175	4	66.7	17	6	ADA61919	Ada61919	NfKb	esse
103	5	83.3	378	7	ADB94794	Adb94794	Programme	176	4	66.7	17	6	ADA61920	Ada61920	NfKb	esse
104	5	83.3	452	4	AAM933545	Aam933545	Human pol	177	4	66.7	17	6	ADA61931	Ada61931	NfKb	esse
105	5	83.3	501	6	ABR92162	Abr92162	Human cer	178	4	66.7	18	5	AAM48628	Aam48628	Anti-infl	
106	5	83.3	597	4	ABB62635	Abb62635	Drosophil	179	4	66.7	18	5	AAM48632	Aam48632	Anti-infl	
107	5	83.3	745	5	ABB77291	Abb77291	Human IKK	180	4	66.7	18	5	AAM48633	Aam48633	Anti-infl	
108	5	83.3	745	5	ABB77292	Abb77292	Human IKK	181	4	66.7	18	5	AAM48629	Aam48629	Anti-infl	
109	5	83.3	756	5	ABB77308	Abb77308	Human IKK	182	4	66.7	18	6	ADA61924	Ada61924	NfKb	esse
110	5	83.3	756	5	ABB77309	Abb77309	Human IKK	183	4	66.7	18	6	ADA61904	Ada61904	NfKb	esse
111	5	83.3	1005	5	ABB93598	Abb93598	Herbicida	184	4	66.7	18	6	ADA61908	Ada61908	NfKb	esse
112	5	83.3	5435	4	AAE10145	Aae10145	Streptomy	185	4	66.7	18	6	ADA61905	Ada61905	NfKb	esse
113	4	66.7	5	2	AAR12717	Aar12717	Pentapept	186	4	66.7	18	6	ADA61922	Ada61922	NfKb	esse
114	4	66.7	5	2	AAR51581	Aar51581	Mimotope	187	4	66.7	18	6	ADA61909	Ada61909	NfKb	esse
115	4	66.7	5	2	AAR69949	Aar69949	Pentameri	188	4	66.7	21	2	AAW16213	Aaw16213	Peptide c	
116	4	66.7	5	2	AAR98695	Aar98695	Peptide 7	189	4	66.7	21	2	AAW68846	Aaw68846	Peptide b	
117	4	66.7	117	6	ABB08725	Abb08725	IKKbeta N	190	4	66.7	21	2	AAW58334	Aaw58334	IL-1RtI b	
118	4	66.7	6	5	AAM48655	Aam48655	NBD mutan	191	4	66.7	21	2	AAAY09982	Aay09982	Interleuk	
119	4	66.7	6	5	AAM48530	Aam48530	Anti-infl	192	4	66.7	21	3	ABAB17762	Aab17762	IL-1 anta	
120	4	66.7	6	5	AAM48530	Aam48530	Human NEM	193	4	66.7	21	5	ABB72658	Abb72658	Interleuk	
121	4	66.7	6	6	ABU08418	Abu08418	Human NEM	194	4	66.7	22	5	AAM48630	Aam48630	Anti-infl	
122	4	66.7	6	6	ADA61806	Ada61806	NfKb esse	195	4	66.7	22	5	AAM48634	Aam48634	Anti-infl	
123	4	66.7	7	6	ADA61776	Ada61776	IKKbeta N	196	4	66.7	22	5	AAM48631	Aam48631	Anti-infl	
124	4	66.7	7	4	AAM45417	Aam45417	H11 bindi	197	4	66.7	22	5	AAM48635	Aam48635	Anti-infl	
125	4	66.7	7	5	AAW45422	Aam45422	H11 bindi	198	4	66.7	22	5	AAM48637	Aam48637	Anti-infl	
126	4	66.7	8	5	AAW48535	Aam48535	Anti-infl	199	4	66.7	22	5	AAM48636	Aam48636	Anti-infl	
127	4	66.7	8	5	AAW48527	Aam48527	Anti-infl	200	4	66.7	22	6	ABJ38777	Abj38777	Human G-p	
128	4	66.7	8	6	ADA61810	Ada61810	NfKb esse	201	4	66.7	22	6	ADA61912	Ada61912	NfKb esse	
129	4	66.7	8	6	ADA61803	Aaw96182	IKK-alpha	202	4	66.7	22	6	ADA61907	Ada61907	NfKb esse	
130	4	66.7	9	2	AAW96182	Abg60423	Selective	203	4	66.7	22	6	ADA61926	Ada61926	NfKb esse	
131	4	66.7	9	5	AAW48533	Aam48533	Anti-infl	204	4	66.7	22	6	ADA61911	Ada61911	NfKb esse	
132	4	66.7	9	5	AAW48533	Aam48532	Anti-infl	205	4	66.7	22	6	ADA61923	Ada61923	NfKb esse	
133	4	66.7	9	5	AAW48532	Aam48526	Anti-infl	206	4	66.7	22	6	ADA61906	Ada61906	NfKb esse	
134	4	66.7	9	5	AAW48526	Aam48529	Anti-infl	207	4	66.7	22	6	ADA61913	Ada61913	NfKb esse	
135	4	66.7	9	5	AAW48529	Aam48529	Anti-infl	208	4	66.7	22	6	ADA61910	Ada61910	NfKb esse	
136	4	66.7	9	6	ABR56837	Abr56837	Beta-3 in	209	4	66.7	22	6	ADA61925	Ada61925	NfKb esse	
137	4	66.7	9	6	ADA61808	Ada61808	NfKb esse	210	4	66.7	25	4	AAM38474	Aam38474	Peptide #	
138	4	66.7	9	6	ADA61809	Ada61809	NfKb esse	211	4	66.7	25	4	AAM78216	Aam78216	Human bon	
139	4	66.7	9	6	ADA61802	Ada61802	NfKb esse	212	4	66.7	25	4	AAM65575	Aam65575	Human bra	
140	4	66.7	9	6	ADA61805	Ada61805	NfKb esse	213	4	66.7	25	4	ABG59863	Abg59863	Human liv	
141	4	66.7	10	5	ABB77313	Abb77313	IKKbeta N	214	4	66.7	25	5	ABG47227	Abg47227	Human pep	
142	4	66.7	10	5	AAW48531	Aam48531	Anti-infl	215	4	66.7	26	4	AAG73284	Aag73284	Conserved	
143	4	66.7	10	5	AAW48528	Aam48528	Anti-infl	216	4	66.7	28	5	ABB08740	Aab08740	IKKbeta N	
144	4	66.7	10	6	ADA61804	Ada61804	NfKb esse	217	4	66.7	28	5	AAM48523	Aam48523	NBD pepti	
145	4	66.7	10	6	ADA61807	Ada61807	NfKb esse	218	4	66.7	28	6	ABU08434	Abu08434	Wild-type	
146	4	66.7	11	5	ABB77311	Abb77311	Human NBD	219	4	66.7	28	6	ADA61791	Ada61791	IKKbeta N	
147	4	66.7	11	5	AAM48653	Aam48653	NBD pepti	220	4	66.7	29	6	ADA61936	Ada61936	IKKbeta N	
148	4	66.7	11	5	AAM48525	Aam48525	Anti-infl	221	4	66.7	29	6	ADA04779	Ada04779	IGF-1R bi	
149	4	66.7	11	5	AAM48506	Aam48506	Human IKK	222	4	66.7	35	3	AAG05204	Aag05204	Arabidops	
150	4	66.7	11	6	ADA61938	Ada61938	IKKbeta N	223	4	66.7	36	4	AAG79287	Aag79287	Amino aci	
151	4	66.7	11	6	ADA61801	Ada61801	NfKb esse	224	4	66.7	36	5	AAM48652	Aam48652	IKKbeta m	
152	4	66.7	12	2	AAR93675	Aar93675	HIV princ	225	4	66.7	36	6	ADA04689	Ada04689	IGF-1R bi	
153	4	66.7	12	6	ADA61918	Ada61918	NfKb esse	226	4	66.7	36	6	ABU08436	Abu08436	Human Ika	
154	4	66.7	12	7	ADC28147	Adc28147	Synthetic	227	4	66.7	36	6	ADA61935	Ada61935	IKKbeta N	
155	4	66.7	13	3	AAAY78379	Aay78379	Human pap	228	4	66.7	37	4	AAG79285	Aag79285	Amino aci	
156	4	66.7	13	5	AAM48640	Aam48640	Anti-infl	229	4	66.7	40	3	AAB20707	Aab20707	Polymeric	
157	4	66.7	13	5	AAM48642	Aam48642	Anti-infl	230	4	66.7	42	4	AAM84684	Aam84684	Human imm	
158	4	66.7	13	5	AAM48645	Aam48645	Anti-infl	231	4	66.7	44	2	AAAY12990	Aay12990	Human sec	
159	4	66.7	13	5	AAM48641	Aam48641	Anti-infl	232	4	66.7	45	4	AAM20837	Aam20837	Peptide #	
160	4	66.7	13	6	ADA61921	Ada61921	NfKb esse	233	4	66.7	45	4	ABB42541	Abb42541	Peptide #	
161	4	66.7	13	6	ADA61916	Ada61916	NfKb esse	234	4	66.7	45	4	AAM36354	Aam36354	Peptide #	
162	4	66.7	13	6	ADA61927	Ada61927	NfKb esse	235	4	66.7	45	4	ABB25938	Abb25938	Protein #	
163	4	66.7	13	6	ADA61928	Ada61928	NfKb esse	236	4	66.7	45	4	ABB25938	Abb25938	Protein #	
164	4	66.7	14	4	AAM96947	Aam96947	Human pep	237	4	66.7	45	4	AAM76244	Aam76244	Human bon	
165	4	66.7	14	6	ADA61917	Ada61917	NfKb esse	238	4	66.7	45	4	AAM63429	Aam63429	Human bra	
166	4	66.7	17	5	AAW48638	Aam48638	Anti-infl	239	4	66.7	45	4	ABG57959	Abg57959	Human liv	
167	4	66.7	17	5	AAW48644	Aam48644	Anti-infl	240	4	66.7	45	5	ABG45568	Abg45568	Human pep	
168	4	66.7	17	5	AAW48639	Aam48639	Anti-infl	241	4	66.7	46	6	ABP99569	Abp99569	Human sec	
169	4	66.7	17	5	AAW48643	Aam48643	Anti-infl	242	4	66.7	46	6	ABR01048	AbR01048	Human gen	
170	4	66.7	17	5	ADA61930	Ada61930	NfKb esse	243	4	66.7	47	4	AAB75245	Aab75245	Human sec	
171	4	66.7	17	6				244	4	66.7	51	4	AAM87126	Aam87126	Human imm	
											51	6	ABU07181	Abu07181	Maize SSI	

245	4	66.7	51	6	ABU07187	Abu07187 Maize SSI
246	4	66.7	51	6	ABU07182	Abu07182 Maize SSI
247	4	66.7	52	6	ABU07186	Abu07186 Maize SSI
248	4	66.7	52	6	ABU07179	Abu07179 Maize SSI
249	4	66.7	52	6	ABU07180	Abu07180 Maize SSI
250	4	66.7	52	6	ABU07185	Abu07185 Maize SSI
251	4	66.7	52	6	ABU07184	Abu07184 Maize SSI
252	4	66.7	52	6	ABU07188	Abu07188 Maize SSI
253	4	66.7	53	4	AAU44655	Aau44655 Propionib
254	4	66.7	53	6	ABM41174	Abm41174 Propionib
255	4	66.7	54	4	AAU42648	Aau42648 Propionib
256	4	66.7	54	6	ABM39167	Abm39167 Propionib
257	4	66.7	55	4	AAG79292	Aag79292 Amino aci
258	4	66.7	55	4	AAU52825	Aau52825 Propionib
259	4	66.7	55	6	ABM49344	Abm49344 Propionib
260	4	66.7	56	4	AAG79290	Aag79290 Amino aci
261	4	66.7	59	2	AAU21373	Aay21373 Human HUP
262	4	66.7	60	4	AAO04611	Aao04611 Human pol
263	4	66.7	60	4	ABG30122	Abg30122 Novel hum
264	4	66.7	61	4	AAM80639	Aam80639 Human hae
265	4	66.7	63	6	ABR41192	Abr41192 Human DIT
266	4	66.7	64	4	AAU48905	Aau48905 Propionib
267	4	66.7	64	6	ABM45424	Abm45424 Propionib
268	4	66.7	65	4	AAU49106	Aau49106 Propionib
269	4	66.7	65	6	ABM45625	Abm45625 Propionib
270	4	66.7	66	4	AAU64373	Aau64373 Propionib
271	4	66.7	66	6	ABM60892	Abm60892 Propionib
272	4	66.7	67	4	AAM94937	Aam94937 Human rep
273	4	66.7	67	4	AAU45676	Aau45676 Propionib
274	4	66.7	67	4	AAU39116	Aau39116 Propionib
275	4	66.7	67	6	ABM42195	Abm42195 Propionib
276	4	66.7	67	6	ABM35635	Abm35635 Propionib
277	4	66.7	68	2	AAU12500	Aay12500 Human 5'
278	4	66.7	68	3	AAG56793	Aag56793 Arabidops
279	4	66.7	68	3	AAG60376	Aag60376 Arabidops
280	4	66.7	68	4	ABG28346	Abg28346 Novel hum
281	4	66.7	71	4	AAU51730	Aau51730 Propionib
282	4	66.7	71	6	ABM48249	Abm48249 Propionib
283	4	66.7	73	4	ABG29252	Abg29252 Novel hum
284	4	66.7	74	2	AAR40036	Aar40036 Filistata
285	4	66.7	74	4	AAG76325	Aag76325 Human col
286	4	66.7	74	4	AAU52761	Aau52761 Propionib
287	4	66.7	74	6	ABM49280	Abm49280 Propionib
288	4	66.7	75	4	AAU59041	Aau59041 Propionib
289	4	66.7	75	6	ABM55560	Abm55560 Propionib
290	4	66.7	75	6	ABU07239	Abu07239 Maize Dul
291	4	66.7	76	3	AAG12524	Aag12524 Zea mays
292	4	66.7	77	5	ABB97840	Abb97840 Human sec
293	4	66.7	77	5	ABB97927	Abb97927 Human sec
294	4	66.7	81	4	AAO07074	Aao07074 Human pol
295	4	66.7	82	3	AAU96460	Aay96460 Partial r
296	4	66.7	82	4	AAM23897	Aam23897 Human EST
297	4	66.7	82	4	AAB80626	Aab80626 Environme
298	4	66.7	82	5	AAE21195	Aae21195 Human gen
299	4	66.7	82	5	ABG64851	Abg64851 Human alb
300	4	66.7	82	6	ADA56952	Ada56952 Human sec
301	4	66.7	82	6	ADA40803	Ada40803 Human sec
302	4	66.7	83	4	AAU53907	Aau53907 Propionib
303	4	66.7	83	6	ABM50426	Abm50426 Propionib
304	4	66.7	84	2	AAU33719	Aay33719 Human p10
305	4	66.7	84	4	ABB17259	Abb17259 Human ner
306	4	66.7	86	2	AAU36020	Aay36020 Extended
307	4	66.7	87	5	ABB97836	Abb97836 Human sec
308	4	66.7	88	5	ABP01735	Abp01735 Human ORF
309	4	66.7	88	6	ABU00805	Abu00805 S. pneumo
310	4	66.7	90	4	AAU40365	Aau40365 Propionib
311	4	66.7	90	5	ABJ10366	Abj10366 Human bre
312	4	66.7	90	6	ABM36884	Abm36884 Propionib
313	4	66.7	93	4	AAO03124	Aao03124 Human pol
314	4	66.7	94	4	AAM21117	Aam21117 Peptide #
315	4	66.7	94	4	ABB43432	Abb43432 Peptide #
316	4	66.7	94	4	AAM37320	Aam37320 Peptide #
317	4	66.7	94	4	ABB26403	Abb26403 Protein #

318	4	66.7	94	4	AAM77186	Aam77186 Human bon
319	4	66.7	94	4	AAM64361	Aam64361 Human bra
320	4	66.7	94	4	ABG58809	Abg58809 Human liv
321	4	66.7	94	4	ABG17509	Abg17509 Novel hum
322	4	66.7	94	4	ABG17547	Abg17547 Novel hum
323	4	66.7	94	5	ABG46199	Abg46199 Human pep
324	4	66.7	94	6	ABP75436	Abp75436 Human sec
325	4	66.7	95	4	AAM89228	Aam89228 Human imm
326	4	66.7	95	6	ABR58357	Abr58357 Bcu1040 p
327	4	66.7	96	5	ABB10043	Abb10043 Human glu
328	4	66.7	98	4	AAM95858	Aam95858 Human rep
329	4	66.7	98	4	ABB96389	Abb96389 Human tes
330	4	66.7	99	2	AAR07302	Aar07302 C-termina
331	4	66.7	99	4	AAM95002	Aam95002 Human rep
332	4	66.7	99	4	ABB95710	Abb95710 Human tes
333	4	66.7	101	4	AAU59343	Aau59343 Propionib
334	4	66.7	101	4	AAU62311	Aau62311 Propionib
335	4	66.7	101	6	ADA54754	Ada54754 Human pro
336	4	66.7	101	6	ABM55862	Abm55862 Propionib
337	4	66.7	101	6	ABM58830	Abm58830 Propionib
338	4	66.7	103	2	AAU06339	Aay06339 Gliocladi
339	4	66.7	105	4	ABG10964	Abg10964 Novel hum
340	4	66.7	106	4	AAM84073	Aam84073 Human imm
341	4	66.7	108	2	AAW34219	Aaw34219 Streptomy
342	4	66.7	108	2	AAW55820	Aaw55820 Streptomy
343	4	66.7	109	2	AAR07399	Aar07399 Chlamydia
344	4	66.7	109	3	AAG12523	Aag12523 Zea mays
345	4	66.7	112	5	ABP07121	Abp07121 Human ORF
346	4	66.7	112	5	AAM49275	Aam49275 Human cel
347	4	66.7	114	5	ABB89701	Abb89701 Human pol
348	4	66.7	115	4	AAU19524	Aau19524 Human dia
349	4	66.7	115	4	ABG02552	Abg02552 Novel hum
350	4	66.7	115	5	AAM49160	Aam49160 Human ubi
351	4	66.7	116	5	ABP09847	Abp09847 Human ORF
352	4	66.7	117	4	AAB93851	Aab93851 Human pro
353	4	66.7	117	5	ABG95220	Abg95220 Human nov
354	4	66.7	117	6	ABO34414	Abc34414 Region of
355	4	66.7	118	4	AAU49158	Aau49158 Propionib
356	4	66.7	118	4	AAG64019	Aag64019 Human ute
357	4	66.7	118	4	ABG02037	Abg02037 Novel hum
358	4	66.7	118	6	ABM45677	Abm45677 Propionib
359	4	66.7	118	7	ADC01192	Adc01192 Enterohae
360	4	66.7	119	7	ADB65107	Adb65107 Human pro
361	4	66.7	120	4	AAU31645	Aau31645 Novel hum
362	4	66.7	121	2	AAU60003	Aay60003 Human end
363	4	66.7	122	3	AAG03672	Aag03672 Human sec
364	4	66.7	122	4	AAG73933	Aag73933 Human col
365	4	66.7	122	6	ABR39289	Abr39289 Protein s
366	4	66.7	122	7	ADB65781	Adb65781 Human pro
367	4	66.7	124	3	AAG12522	Aag12522 Zea mays
368	4	66.7	125	4	ABG05086	Abg05086 Novel hum
369	4	66.7	128	7	ADD19155	Add19155 Lilium as
370	4	66.7	135	5	ABP34075	Abp34075 Human ORF
371	4	66.7	135	6	ABU05089	Abu05089 Human exp
372	4	66.7	137	6	ABP80191	Abp80191 N. gonorr
373	4	66.7	139	3	AAU64683	Aay64683 Human 5'
374	4	66.7	140	4	AAU16426	Aau16426 Human nov
375	4	66.7	140	4	AAG78872	Aag78872 Human DNA
376	4	66.7	140	4	ABG15558	Abg15558 Novel hum
377	4	66.7	140	6	ABU55495	Abu55495 Human nov
378	4	66.7	141	2	AAU73883	Aay73883 Human pro
379	4	66.7	141	2	AAU59770	Aay59770 Human nor
380	4	66.7	144	3	AAB25420	Aab25420 Pinus rad
381	4	66.7	144	6	ABU19018	Abu19018 Protein e
382	4	66.7	145	4	ABG09589	Abg09589 Novel hum
383	4	66.7	145	6	ABP75609	Abp75609 Human sec
384	4	66.7	146	6	ABU18616	Abu18616 Protein e
385	4	66.7	150	4	AAU59042	Aau59042 Propionib
386	4	66.7	150	4	ABG15892	Abg15892 Novel hum
387	4	66.7	150	6	ABM55561	Abm55561 Propionib
388	4	66.7	151	2	AAU59765	Aay59765 Human nor
389	4	66.7	151	4	AAM80326	Aam80326 Human hae
390	4	66.7	153	3	AAB43922	Aab43922 Human can

Aam77186	Human	boa
Aam64361	Human	bra
Abg58809	Human	liv
Abg17547	Novel	hum
Abg17547	Novel	hum
Abg46199	Human	pep
Abp75436	Human	sec
Aam89228	Human	imm
Abr58357	Bcu1040	p
Abb10043	Human	glu
Aam95858	Human	rep
Abb96389	Human	tes
Aar07302	C-termina	
Aam95002	Human	rep
Abb95710	Human	tes
Aau59343	Propionib	
Aau62311	Propionib	
Ada54754	Human	pro
Abm55862	Propionib	
Abm58830	Propionib	
Aay06339	Gliocladi	
Abg10964	Novel	hum
Aam84073	Human	imm
Aaw34219	Streptomy	
Aaw55820	Streptomy	
Aar07399	Chlamydia	
Aag12523	Zea mays	
Abp07121	Human	ORF
Aam49275	Human	cel
Abb89701	Human	pol
Aau19524	Human	dia
Abg02552	Novel	hum
Aam49160	Human	ubi
Abp09847	Human	ORF
Abg93851	Human	pro
Abg95220	Human	nov
Abo33414	Region of	
Aau49158	Propionib	
Aag64019	Human	ute
Abg02037	Novel	hum
Abm45677	Propionib	
Adc01192	Enterohae	
Adb65107	Human	pro
Aau31645	Novel	hum
Aay60003	Human	end
Aag03672	Human	sec
Abr39233	Human	col
Abg39289	Protein s	
Adb65781	Human	pro
Aag12522	Zea mays	
Abg05086	Novel	hum
Add19155	Lilium as	
Abp34075	Human	ORF
Abu05089	Human	exp
Abp80191	N. gonorr	
Aay64683	Human 5'	
Aau16426	Human	nov
Aag78872	Human	DNA
Abg15558	Novel	hum
Abu55495	Human	nov
Aay73883	Human	pro
Aay59770	Human	nor
Aab25420	Pinus rad	
Abu19018	Protein e	
Abg09589	Novel	hum
Abp75609	Human	sec
Abu18616	Protein e	
Aau59042	Propionib	
Abg15892	Novel	hum
Abm55561	Propionib	
Aay59765	Human	nor
Aam59326	Human	hae
Aab43922	Human	can

391	4	66.7	154	4	AAB63563	Aab63563 Human gas	464	4	66.7	246	6	ABU02373	Abu02373 S. pneumo
392	4	66.7	158	4	ABG11618	Abg11618 Novel hum	465	4	66.7	247	2	AAW38504	Aaw38504 Streptoco
393	4	66.7	160	4	AAU43406	Aau43406 Propionib	466	4	66.7	247	2	AAU85933	Aay85933 S. pneumo
394	4	66.7	160	6	ABM39925	Abm39925 Propionib	467	4	66.7	247	4	AAU37868	Aau37868 Streptoco
395	4	66.7	160	6	ABU40249	Abu40249 Protein e	468	4	66.7	247	4	AAU38029	Aau38029 Streptoco
396	4	66.7	163	2	AAR91595	Aar91595 PR-1 like	469	4	66.7	247	4	ABB71338	Abb71338 Drosophil
397	4	66.7	163	2	AAU29944	Aay29944 Zea mays	470	4	66.7	247	6	ABU02263	Abu02263 S. pneumo
398	4	66.7	164	6	ABR47872	Abr47872 Human sec	471	4	66.7	247	6	ABU44315	Abu44315 Protein e
399	4	66.7	164	6	ABR00141	Abr00141 Human gen	472	4	66.7	249	5	ABP26263	Abp26263 Streptoco
400	4	66.7	164	7	ADB91628	Adb91628 Human sec	473	4	66.7	249	6	ABU46851	Abu46851 Protein e
401	4	66.7	164	7	ADC74263	Adc74263 Human sec	474	4	66.7	250	4	AAG91045	Aag91045 C glutami
402	4	66.7	166	4	AAM93883	Aam93883 Human pol	475	4	66.7	251	6	ABU46217	Abu46217 Protein e
403	4	66.7	167	4	AAU19622	Aau19622 Human dia	476	4	66.7	253	1	AAP70569	Aap70569 Sequence
404	4	66.7	168	6	ADA54238	Ada54238 Human pro	477	4	66.7	255	6	ABU23177	Abu23177 Protein e
405	4	66.7	169	4	ABB69952	Abb69952 Drosophil	478	4	66.7	257	5	ABU05566	Abu05566 M. tuberc
406	4	66.7	170	2	AAU29215	Aay29215 Amino aci	479	4	66.7	258	4	ABG18737	Abg18737 Novel hum
407	4	66.7	172	3	AAU96470	Aay96470 Rice gamm	480	4	66.7	259	4	AAM23532	Aam23532 Human EST
408	4	66.7	175	4	ABB69153	Abb69153 Drosophil	481	4	66.7	260	4	AAM25252	Aam25252 Human pro
409	4	66.7	178	6	ABU38927	Abu38927 Protein e	482	4	66.7	260	4	AAM42168	Aam42168 Human pol
410	4	66.7	179	2	AAU19847	Aay19847 B. burgdo	483	4	66.7	262	2	AAW27262	Aaw27262 Plant ste
411	4	66.7	179	4	ABG21335	Abg21335 Novel hum	484	4	66.7	262	3	AAG29276	Aag29276 Arabidops
412	4	66.7	184	2	AAU19849	Aay19849 B. burgdo	485	4	66.7	262	6	ABP71247	Abp71247 A. thalia
413	4	66.7	188	4	AAU30685	Aau30685 Novel hum	486	4	66.7	266	3	AAG51383	Aag51383 Arabidops
414	4	66.7	190	2	AAU36030	Aay36030 Extended	487	4	66.7	266	3	AAG07858	Aag07858 Arabidops
415	4	66.7	190	2	AAU35924	Aay35924 Extended	488	4	66.7	266	4	ABG09483	Abg09483 Novel hum
416	4	66.7	190	4	AAM40382	Aam40382 Human pol	489	4	66.7	272	5	ABP26244	Abp26244 Streptoco
417	4	66.7	190	6	ABR39942	Abr39942 Human pro	490	4	66.7	272	5	AAO20952	Aao20952 Human-N-k
418	4	66.7	191	3	AAU96459	Aay96459 Corn gamm	491	4	66.7	272	6	ABG76399	Abg76399 Amino aci
419	4	66.7	195	6	ADA55707	Ada55707 Human pro	492	4	66.7	272	7	ADC95914	Adc95914 E. faeciu
420	4	66.7	199	4	ABG05956	Abg05956 Novel hum	493	4	66.7	273	4	ABG11759	Abg11759 Novel hum
421	4	66.7	202	7	ADB64582	Adb64582 Human pro	494	4	66.7	273	6	ABU38161	Abu38161 Protein e
422	4	66.7	203	2	AAU19846	Aay19846 B. burgdo	495	4	66.7	273	6	ABU37457	Abu37457 Protein e
423	4	66.7	203	2	AAU19848	Aay19848 B. burgdo	496	4	66.7	276	3	AAG09067	Aag09067 Arabidops
424	4	66.7	204	3	AAU36057	Aag36057 Zea mays	497	4	66.7	280	4	AAG81234	Aag81234 Mycobacte
425	4	66.7	206	4	ABB12052	Abb12052 Human dJ8	498	4	66.7	280	6	ABP96396	Abp96396 Anabaena
426	4	66.7	206	6	ABP75868	Abp75868 Human sec	499	4	66.7	280	6	ABP96395	Abp96395 Nostoc pu
427	4	66.7	207	3	AAG29277	Aag29277 Arabidops	500	4	66.7	280	7	ADD19157	Add19157 Anabaena
428	4	66.7	207	6	ABU00213	Abu00213 Human nov	501	4	66.7	280	7	ADD19156	Add19156 Nostoc pu
429	4	66.7	209	4	ABG29051	Abg29051 Novel hum	502	4	66.7	281	4	ABG02036	Abg02036 Novel hum
430	4	66.7	210	4	ABG03371	Abg03371 Novel hum	503	4	66.7	281	6	ABP56488	Abp56488 Human D-a
431	4	66.7	210	5	ABP42048	Abp42048 Human ova	504	4	66.7	281	7	AAO29691	Aao29691 Human D-a
432	4	66.7	213	4	AAE00717	Aae00717 Rice BCS1	505	4	66.7	282	3	AAG09066	Aag09066 Arabidops
433	4	66.7	213	4	AAG67279	Aag67279 Amino aci	506	4	66.7	284	6	ABJ18778	Abj18778 Pseudomon
434	4	66.7	215	5	ABB83844	Abb83844 Human end	507	4	66.7	285	5	ABB97188	Abb97188 Novel hum
435	4	66.7	217	7	ADC96623	Adc96623 E. faeciu	508	4	66.7	285	6	ABU04665	Abu04665 Human exp
436	4	66.7	220	4	AAB94488	Aab94488 Human pro	509	4	66.7	286	3	AAU32304	Aay32304 Corn acid
437	4	66.7	220	6	ABP56486	Abp56486 Human D-a	510	4	66.7	287	6	ABP79668	Abp79668 N. gonorr
438	4	66.7	220	7	AAO29689	Aao29689 Human D-a	511	4	66.7	290	4	ABG03255	Abg03255 Novel hum
439	4	66.7	223	2	AAW63025	Aaw63025 Theileria	512	4	66.7	292	4	ABG24161	Abg24161 Novel hum
440	4	66.7	224	5	ABP41334	Abp41334 Human ova	513	4	66.7	293	3	AAU96463	Aay96463 Partial w
441	4	66.7	225	6	ABU25760	Abu25760 Protein e	514	4	66.7	294	6	ABU06977	Abu06977 Maize Sta
442	4	66.7	231	4	ABG12209	Abg12209 Novel hum	515	4	66.7	295	2	AAR05562	Aar05562 Laminin -
443	4	66.7	234	4	AAU51001	Aau51001 Propionib	516	4	66.7	295	5	ABB57248	Abb57248 Mouse isc
444	4	66.7	234	6	ABM47520	Abm47520 Propionib	517	4	66.7	295	6	ABU04658	Abu04658 Human exp
445	4	66.7	235	4	AAU52773	Aau52773 Propionib	518	4	66.7	295	6	ABU04655	Abu04655 Human exp
446	4	66.7	235	6	ABM49292	Abm49292 Propionib	519	4	66.7	295	6	ABU04656	Abu04656 Human exp
447	4	66.7	237	4	ABG19300	Abg19300 Novel hum	520	4	66.7	295	6	ABU04659	Abu04659 Human exp
448	4	66.7	237	5	ABB49218	Abb49218 Listeria	521	4	66.7	295	6	ABU04662	Abu04662 Human exp
449	4	66.7	237	6	ABU32764	Abu32764 Protein e	522	4	66.7	295	6	ABU04660	Abu04660 Human exp
450	4	66.7	238	2	AAU06361	Aay06361 Gliocladi	523	4	66.7	295	6	ABU04667	Abu04667 Human exp
451	4	66.7	238	3	AAU84339	Aay84339 Amino aci	524	4	66.7	295	6	ABU04672	Abu04672 Human exp
452	4	66.7	238	3	AAB14874	Aab14874 Gliocladi	525	4	66.7	295	6	ABU04670	Abu04670 Human exp
453	4	66.7	238	5	AAU77582	Aau77582 G. roseum	526	4	66.7	295	6	ABU04657	Abu04657 Human exp
454	4	66.7	238	5	AAU77426	Aau77426 Gliocladi	527	4	66.7	295	6	ABU04673	Abu04673 Human exp
455	4	66.7	239	2	AAU06353	Aay06353 Aspergill	528	4	66.7	295	6	ABU04664	Abu04664 Human exp
456	4	66.7	239	3	AAU84331	Aay84331 Amino aci	529	4	66.7	295	6	ABU04661	Abu04661 Human exp
457	4	66.7	239	3	AAB14866	Aab14866 Aspergill	530	4	66.7	295	6	ABU04671	Abu04671 Human exp
458	4	66.7	239	5	AAU77574	Aau77574 A. kawach	531	4	66.7	296	4	AAG72643	Aag72643 Murine OR
459	4	66.7	239	5	AAU77418	Aau77418 Aspergill	532	4	66.7	297	4	ABG18736	Abg18736 Novel hum
460	4	66.7	241	4	ABG25707	Abg25707 Novel hum	533	4	66.7	298	2	AAR13982	Aar13982 Geranylge
461	4	66.7	243	4	ABG17504	Abg17504 Novel hum	534	4	66.7	298	2	AAW01120	Aaw01120 Recombina
462	4	66.7	246	5	ABP26262	Abp26262 Streptoco	535	4	66.7	298	2	AAW00171	Aaw00171 N termina
463	4	66.7	246	5	ABP60839	Abp60839 Caenorhab	536	4	66.7	298	2	AAW00342	Aaw00342 N-termina

537	4	66.7	298	2	AAW32470	Aaw32470 Erwinia h	610	4	66.7	308	7	ADB17997	Adb17997 Human PRO
538	4	66.7	298	5	AAO15511	Aao15511 Agromyces	611	4	66.7	308	7	ADA86680	Ada86680 Novel hum
539	4	66.7	299	3	AAG22906	Aag22906 Arabidops	612	4	66.7	308	7	ADA87783	Ada87783 Novel hum
540	4	66.7	299	5	ABB90876	Abb90876 Herbicida	613	4	66.7	308	7	ADA46171	Ada46171 Novel hum
541	4	66.7	300	2	AAR07532	Aar07532 Modified	614	4	66.7	308	7	ADB28201	Adb28201 Human PRO
542	4	66.7	300	6	ABU04666	Abu04666 Human exp	615	4	66.7	308	7	ADB28753	Adb28753 Human PRO
543	4	66.7	301	6	ABP96390	Abp96390 Brassica	616	4	66.7	308	7	ADA76705	Ada76705 Human PRO
544	4	66.7	301	6	ABP96389	Abp96389 Brassica	617	4	66.7	308	7	ADA88335	Ada88335 Novel hum
545	4	66.7	302	4	ABG11344	Abg11344 Novel hum	618	4	66.7	308	7	ADA97340	Ada97340 Human PRO
546	4	66.7	305	6	ABP96394	Abp96394 Zea mays	619	4	66.7	308	7	ADB27097	Adb27097 Human PRO
547	4	66.7	306	7	AAE00227	Aae00227 Protein e	620	4	66.7	308	7	ADB22030	Adb22030 Novel hum
548	4	66.7	306	7	ADB91913	Adb91913 Acyltrans	621	4	66.7	308	7	ADA66721	Ada66721 Human PRO
549	4	66.7	307	2	AAR13981	Aar13981 Geranylge	622	4	66.7	308	7	ADB22582	Adb22582 Human PRO
550	4	66.7	307	2	AAW01119	Aaw01119 Geranylge	623	4	66.7	308	7	ADB23355	Adb23355 Human PRO
551	4	66.7	307	2	AAW00170	Aaw00170 Geranylge	624	4	66.7	308	7	ADA92077	Ada92077 Novel hum
552	4	66.7	307	2	AAW00341	Aaw00341 Wild type	625	4	66.7	308	7	ADB15140	Adb15140 Human PRO
553	4	66.7	307	2	AAW32469	Aaw32469 Geranylge	626	4	66.7	308	7	ADB38392	Adb38392 Novel hum
554	4	66.7	307	4	ABB64446	Abb64446 Drosophil	627	4	66.7	308	7	ADB37840	Adb37840 Novel hum
555	4	66.7	307	5	ABP69089	Abp69089 Human pol	628	4	66.7	308	7	ADB66312	Adb66312 Novel hum
556	4	66.7	308	3	AAG07857	Aag07857 Arabidops	629	4	66.7	308	7	ADB89392	Adb89392 Human PRO
557	4	66.7	308	3	AGS51382	Ags51382 Arabidops	630	4	66.7	308	7	ADB90124	Adb90124 Human PRO
558	4	66.7	308	4	AAU12221	Aau12221 Human PRO	631	4	66.7	308	7	ADB39225	Adb39225 Novel hum
559	4	66.7	308	6	ABO17665	Abol17665 Novel hum	632	4	66.7	308	7	ADB46848	Adb46848 Novel hum
560	4	66.7	308	6	ABU80919	Abu80919 Human PRO	633	4	66.7	308	7	ADB86455	Adb86455 Human PRO
561	4	66.7	308	6	ABU66619	Abu66619 Human PRO	634	4	66.7	308	7	ADB77060	Adb77060 Novel hum
562	4	66.7	308	6	ABU59700	Abu59700 Novel sec	635	4	66.7	308	7	ADB34217	Adb34217 Human PRO
563	4	66.7	308	6	ABO24890	Abol24890 Human sec	636	4	66.7	308	7	ADB35321	Adb35321 Human PRO
564	4	66.7	308	6	ABU66895	Abu66895 Human sec	637	4	66.7	308	7	ADB33665	Adb33665 Human PRO
565	4	66.7	308	6	ADA45619	Ada45619 Novel hum	638	4	66.7	308	7	ADB34769	Adb34769 Human PRO
566	4	66.7	308	6	ADA76050	Ada76050 Human PRO	639	4	66.7	308	7	ADB35873	Adb35873 Human PRO
567	4	66.7	308	6	ADA18700	Ada18700 Human PRO	640	4	66.7	308	7	ADB46268	Adb46268 Novel hum
568	4	66.7	308	6	ADA61323	Ada61323 Homo sapi	641	4	66.7	308	7	ADC50141	Adc50141 Novel hum
569	4	66.7	308	6	ADB19108	Adb19108 Novel hum	642	4	66.7	308	7	ADC71688	Adc71688 Novel hum
570	4	66.7	308	6	ADB27649	Adb27649 Human PRO	643	4	66.7	308	7	ADC59667	Adc59667 Novel hum
571	4	66.7	308	6	ADA86128	Ada86128 Novel hum	644	4	66.7	308	7	ADC52674	Adc52674 Novel hum
572	4	66.7	308	6	ADB15692	Adb15692 Human PRO	645	4	66.7	308	7	ADC57028	Adc57028 Novel hum
573	4	66.7	308	6	ADA47478	Ada47478 Human PRO	646	4	66.7	308	7	ADC60219	Adc60219 Novel hum
574	4	66.7	308	6	ADA67273	Ada67273 Human PRO	647	4	66.7	308	7	ADC50694	Adc50694 Novel hum
575	4	66.7	308	6	ADB30280	Adb30280 Human PRO	648	4	66.7	308	7	ADC65221	Adc65221 Human PRO
576	4	66.7	308	6	ADA85576	Ada85576 Novel hum	649	4	66.7	308	7	ADC54319	Adc54319 Novel hum
577	4	66.7	308	6	ADA96788	Ada96788 Human PRO	650	4	66.7	308	7	ADC53280	Adc53280 Novel hum
578	4	66.7	308	6	ADA79092	Ada79092 Human PRO	651	4	66.7	308	7	ADC58803	Adc58803 Novel hum
579	4	66.7	308	6	ADA87231	Ada87231 Novel hum	652	4	66.7	308	7	ADC55681	Adc55681 Novel hum
580	4	66.7	308	6	ADB16433	Adb16433 Human PRO	653	4	66.7	308	7	ADC58251	Adc58251 Novel hum
581	4	66.7	308	6	ADA91525	Ada91525 Novel hum	654	4	66.7	308	7	ADD02925	Add02925 Novel hum
582	4	66.7	308	6	ADB14588	Adb14588 Human PRO	655	4	66.7	308	7	ADC89917	Adc89917 Novel hum
583	4	66.7	308	6	ADB18549	Adb18549 Novel hum	656	4	66.7	308	7	ADC69336	Adc69336 Human PRO
584	4	66.7	308	6	ADA93764	Ada93764 Human PRO	657	4	66.7	308	7	ADC48225	Adc48225 Human PRO
585	4	66.7	308	6	ADB19660	Adb19660 Novel hum	658	4	66.7	308	7	ADD09754	Add09754 Human PRO
586	4	66.7	308	6	ADB12972	Adb12972 Human PRO	659	4	66.7	308	7	ADD04329	Add04329 Novel hum
587	4	66.7	308	6	ABO43198	Abol43198 Novel hum	660	4	66.7	308	7	ADC80285	Adc80285 Novel hum
588	4	66.7	308	6	ADA74226	Ada74226 Human PRO	661	4	66.7	308	7	ADD10792	Add10792 Human PRO
589	4	66.7	308	6	ADB24459	Adb24459 Human PRO	662	4	66.7	308	7	ADC47673	Adc47673 Human PRO
590	4	66.7	308	6	ADA81983	Ada81983 Human PRO	663	4	66.7	308	7	ADC79733	Adc79733 Novel hum
591	4	66.7	308	6	ADA74946	Ada74946 Human PRO	664	4	66.7	308	7	ADD09202	Add09202 Human PRO
592	4	66.7	308	6	ADA85024	Ada85024 Novel hum	665	4	66.7	308	7	ADD40915	Add40915 Novel hum
593	4	66.7	308	6	ADA84472	Ada84472 Novel hum	666	4	66.7	308	7	ADD52054	Add52054 Human PRO
594	4	66.7	308	6	ADB29728	Adb29728 Human PRO	667	4	66.7	308	7	ADD52794	Add52794 Human PRO
595	4	66.7	308	6	ADA80256	Ada80256 Human PRO	668	4	66.7	308	7	ADD53346	Add53346 Novel hum
596	4	66.7	308	6	ADA75498	Ada75498 Human PRO	669	4	66.7	308	7	ADD51502	Add51502 Human PRO
597	4	66.7	308	6	ADA46723	Ada46723 Human PRO	670	4	66.7	308	7	ADD02301	Add02301 Human PRO
598	4	66.7	308	6	ADB25019	Adb25019 Human PRO	671	4	66.7	308	7	ADD01735	Add01735 Human PRO
599	4	66.7	308	6	ADA93195	Ada93195 Human PRO	672	4	66.7	308	7	ADD53917	Add53917 Novel hum
600	4	66.7	308	6	ADB26545	Adb26545 Human PRO	673	4	66.7	308	7	ADD92234	Add92234 Human PRO
601	4	66.7	308	6	ADB30832	Adb30832 Human PRO	674	4	66.7	308	7	ADD91130	Add91130 Human PRO
602	4	66.7	308	6	ADA60760	Ada60760 Homo sapi	675	4	66.7	308	7	ADE03744	Ade03744 Human PRO
603	4	66.7	308	6	ADB23907	Adb23907 Human PRO	676	4	66.7	308	7	ADE32041	Ade32041 Novel hum
604	4	66.7	308	6	ADA96236	Ada96236 Human PRO	677	4	66.7	308	7	ADE21973	Ade21973 Human PRO
605	4	66.7	308	6	ADA80808	Ada80808 Human PRO	678	4	66.7	308	7	ADD79197	Add79197 Human PRO
606	4	66.7	308	6	ADA95684	Ada95684 Human PRO	679	4	66.7	308	7	ADE41733	Ade41733 Human PRO
607	4	66.7	308	6	ADB25993	Adb25993 Human PRO	680	4	66.7	308	7	ADE17550	Ade17550 Human PRO
608	4	66.7	308	6	ADB21478	Adb21478 Novel hum	681	4	66.7	308	7	ADD91682	Add91682 Human PRO
609	4	66.7	308	7	ADA77257	Ada77257 Human PRO	682	4	66.7	308	7	ADE333145	Ade333145 Novel hum

683	4	66.7	308	7	ADE33697	Ade33697	Novel hum	756	4	66.7	346	2	AAR51473	Aar51473	psts gene
684	4	66.7	308	7	ADD79749	Add79749	Human PRO	757	4	66.7	346	2	AAR60641	Aar60641	psts vari
685	4	66.7	308	7	ADD92786	Add92786	Human PRO	758	4	66.7	346	2	AAR60642	Aar60642	psts vari
686	4	66.7	308	7	ADE19206	Ade19206	Human PRO	759	4	66.7	346	2	AAR60643	Aar60643	psts vari
687	4	66.7	308	7	ADE18654	Ade18654	Human PRO	760	4	66.7	346	2	AAR60647	Aar60647	psts vari
688	4	66.7	308	7	ADE42850	Ade42850	Human PRO	761	4	66.7	346	2	AAR60640	Aar60640	psts vari
689	4	66.7	308	7	ADD95639	Add95639	Human PRO	762	4	66.7	346	2	AAR60644	Aar60644	psts vari
690	4	66.7	308	7	ADE22525	Ade22525	Human PRO	763	4	66.7	346	2	AAR60653	Aar60653	psts vari
691	4	66.7	308	7	ADD78643	Add78643	Human PRO	764	4	66.7	346	2	AAR60648	Aar60648	psts vari
692	4	66.7	308	7	ADE32593	Ade32593	Novel hum	765	4	66.7	346	2	AAR60649	Aar60649	psts vari
693	4	66.7	308	7	ADE42285	Ade42285	Human PRO	766	4	66.7	346	2	AAR60651	Aar60651	psts vari
694	4	66.7	308	7	ADD80301	Add80301	Human PRO	767	4	66.7	346	2	AAR60652	Aar60652	psts vari
695	4	66.7	308	7	ADD89329	Add89329	Human PRO	768	4	66.7	346	2	AAR60654	Aar60654	psts vari
696	4	66.7	308	7	ADE40613	Ade40613	Human PRO	769	4	66.7	346	2	AAR60650	Aar60650	psts vari
697	4	66.7	308	7	ADE04412	Ade04412	Human PRO	770	4	66.7	346	4	AAG98332	Aag98332	Escherich
698	4	66.7	308	8	ADC80837	Adc80837	Novel hum	771	4	66.7	347	2	AAW72010	Aaw72010	HSV-2 str
699	4	66.7	308	8	ADD76285	Add76285	Human PRO	772	4	66.7	347	2	AAU68594	Aau68594	Human nov
700	4	66.7	308	8	ADD87649	Add87649	Human PRO	773	4	66.7	347	4	AAU68594	Aau68594	Human nov
701	4	66.7	308	8	ADD86053	Add86053	Human PRO	774	4	66.7	347	4	ABG28895	Abg28895	Novel hum
702	4	66.7	308	8	ADE75501	Ade75501	Human PRO	775	4	66.7	347	6	ABP96381	Abp96381	Brassica
703	4	66.7	308	8	ADE23077	Ade23077	Human PRO	776	4	66.7	347	6	ABP96380	Abp96380	Brassica
704	4	66.7	308	8	ADE23629	Ade23629	Human PRO	777	4	66.7	347	6	ABP56485	Abp56485	Human D-a
705	4	66.7	308	8	ADE24272	Ade24272	Human PRO	778	4	66.7	347	6	ABP56491	Abp56491	Human D-a
706	4	66.7	308	8	ADD87097	Add87097	Human PRO	779	4	66.7	347	6	AAO23078	Aao23078	Human D-a
707	4	66.7	308	8	ADE88963	Ade88963	Human PRO	780	4	66.7	347	6	AAO23074	Aao23074	Human D-a
708	4	66.7	308	8	ADE18102	Ade18102	Human PRO	781	4	66.7	347	6	AAO23075	Aao23075	Human D-a
709	4	66.7	308	8	ADE88411	Ade88411	Human PRO	782	4	66.7	347	7	AAO29694	Aao29694	Human D-a
710	4	66.7	310	5	AAU97833	Aau97833	Fucose-sp	783	4	66.7	347	7	AAO29688	Aao29688	Human D-a
711	4	66.7	310	6	ABP96386	Abp96386	Tagetes e	784	4	66.7	347	7	AAO29697	Aao29697	Alternati
712	4	66.7	310	7	ADD19153	Add19153	Tagetes e	785	4	66.7	347	7	ADD19148	Add19148	Brassica
713	4	66.7	311	6	ABP96393	Abp96393	Tagetes e	786	4	66.7	347	7	ADD19147	Add19147	Brassica
714	4	66.7	313	3	AAG22905	Aag22905	Arabidops	787	4	66.7	348	2	AAW95017	Aaw95017	Arabidops
715	4	66.7	314	4	ABG09396	Abg09396	Novel hum	788	4	66.7	348	3	AAW77937	Aay77937	A. thalia
716	4	66.7	314	6	ABM69332	Abm69332	Photorhab	789	4	66.7	348	3	AAG07856	Aag07856	Arabidops
717	4	66.7	317	2	AAW95016	Aaw95016	Synechocy	790	4	66.7	348	3	AAG51381	Aag51381	Arabidops
718	4	66.7	317	2	AAAY23764	Aay23764	A carboxy	791	4	66.7	348	5	ABH91452	Abh91452	Herbicida
719	4	66.7	317	2	AAAY39338	Aay39338	Carboxyme	792	4	66.7	348	5	AAO17426	Aao17426	A thalian
720	4	66.7	317	3	AAAY56814	Aay56814	T. mariti	793	4	66.7	348	6	ABP96375	Abp96375	A. thalia
721	4	66.7	317	4	AAE08543	Aae08543	Thermotog	794	4	66.7	348	6	ABP96374	Abp96374	A. thalia
722	4	66.7	317	6	ABP56759	Abp56759	T. mariti	795	4	66.7	348	7	ADD19141	Add19141	Arabidops
723	4	66.7	317	6	ABP96397	Abp96397	Synechocy	796	4	66.7	348	7	ADD19142	Add19142	Arabidops
724	4	66.7	319	4	AAG90187	Aag90187	C glutami	797	4	66.7	350	3	AAAY91062	Aay91062	Streptomy
725	4	66.7	319	5	ABP74092	Abp74092	Candida a	798	4	66.7	351	4	AAU23394	Aau23394	Novel hum
726	4	66.7	321	5	ABP28906	Abp28906	Streptoco	799	4	66.7	351	6	AAE35302	Aae35302	Synechocy
727	4	66.7	324	5	AAU76438	Aau76438	Novel des	800	4	66.7	352	3	AAAY96469	Aay96469	Corn gamm
728	4	66.7	325	6	ABU44241	Abu44241	Protein e	801	4	66.7	352	6	ABP96377	Abp96377	Zea mays
729	4	66.7	326	4	ABG25708	Abg25708	Novel hum	802	4	66.7	352	7	ADD19144	Add19144	Zea mays
730	4	66.7	328	3	AAAY84620	Aay84620	Amino aci	803	4	66.7	353	6	ABP78717	Abp78717	N. gonorr
731	4	66.7	329	4	ABG16554	Abg16554	Novel hum	804	4	66.7	354	6	ABP96387	Abp96387	Sorghum b
732	4	66.7	331	6	ABU29037	Abu29037	Protein e	805	4	66.7	354	6	ABU06106	Abu06106	Maize Sta
733	4	66.7	332	3	AAG09065	Aag09065	Arabidops	806	4	66.7	354	6	ABU06106	Abu06106	Sorghum b
734	4	66.7	332	4	ABB64324	Abb64324	Drosophil	807	4	66.7	355	4	AAB79073	Aab79073	Corynebac
735	4	66.7	332	4	ABG02033	Abg02033	Novel hum	808	4	66.7	356	4	ABG07458	Abg07458	Novel hum
736	4	66.7	333	4	AAU19629	Aau19629	Human nov	809	4	66.7	357	4	ABG11207	Abg11207	Novel hum
737	4	66.7	333	5	ABP47849	Abp47849	Human pol	810	4	66.7	360	3	AAAY69157	Aay69157	PeptideA
738	4	66.7	333	7	ADC10811	Adc10811	Human ext	811	4	66.7	361	4	ABG22401	Abg22401	Human nov
739	4	66.7	333	7	ADC94414	Adc94414	E. faeciu	812	4	66.7	362	4	AAAY97745	Aay97745	Human CHR
740	4	66.7	336	2	AAW80692	Aaw80692	S. pneumo	813	4	66.7	362	4	AAE38274	Aae38274	Rice grai
741	4	66.7	336	4	AAU37859	Aau37859	Streptoco	814	4	66.7	362	6	AAE38274	Aae38274	Rice grai
742	4	66.7	336	4	AAM39139	Aam39139	Human pol	815	4	66.7	363	1	AAAP70437	Aap70437	Sequence
743	4	66.7	336	5	AAE24232	Aae24232	Streptomy	816	4	66.7	364	6	ABP96376	Abp96376	Oryza sat
744	4	66.7	336	6	ABP81638	Abp81638	Streptoco	817	4	66.7	364	7	ADD19143	Add19143	Oryza sat
745	4	66.7	336	6	ABU46229	Abu46229	Protein e	818	4	66.7	365	4	AAU47905	Aau47905	Propionib
746	4	66.7	337	3	AAAY80999	Aay80999	S. venezu	819	4	66.7	365	6	ABM44424	Abm44424	Propionib
747	4	66.7	337	3	AAAY77184	Aay77184	S. venezu	820	4	66.7	365	6	ABU25808	Abu25808	Protein e
748	4	66.7	337	3	AAB18651	Aab18651	Amino aci	821	4	66.7	366	3	AAAY96473	Aay96473	Soybean g
749	4	66.7	337	3	AAAY67215	Aay67215	ORF 14 en	822	4	66.7	367	4	ABG11585	Abg11585	Novel hum
750	4	66.7	337	5	ABB90151	Abb90151	Human pol	823	4	66.7	375	7	ADE08292	Ade08292	Novel pro
751	4	66.7	337	6	ABG71675	Abg71675	Protein s	824	4	66.7	381	2	AAW81597	Aaw81597	Protein e
752	4	66.7	337	6	ABG71675	Abg71675	Protein s	825	4	66.7	385	4	ABG00660	Abg00660	Novel hum
753	4	66.7	339	5	ABP41586	Abp41586	Human ova	826	4	66.7	385	6	ABU40381	Abu40381	Protein e
754	4	66.7	343	4	AAU35251	Aau35251	Enterococ	827	4	66.7	386	4	ABG11343	Abg11343	Novel hum
755	4	66.7	346	2	AAR60645	Aar60645	psts vari	828	4	66.7	390	4	ABG01405	Abg01405	Novel hum

829	4	66.7	396	6	ABU34229	Abu34229 Protein e	902	4	66.7	469	6	ABR64168	Abf64168 Aspergill
830	4	66.7	397	4	AAE00850	Aae00850 Human nov	903	4	66.7	469	6	ABR64134	Abf64134 Aspergill
831	4	66.7	398	6	ABG99979	Abg99979 Human nov	904	4	66.7	469	6	ABR64140	Abf64140 Aspergill
832	4	66.7	401	2	AAR10996	Aar10996 Xenopus B	905	4	66.7	469	6	ABR64160	Abf64160 Aspergill
833	4	66.7	402	5	AAO19402	Aao19402 Human mol	906	4	66.7	469	6	ABR64161	Abf64161 Aspergill
834	4	66.7	403	6	ABU96672	Abu96672 Human nuc	907	4	66.7	469	6	ABR64170	Abf64170 Aspergill
835	4	66.7	404	3	AAB32501	Aab32501 S. lavend	908	4	66.7	469	6	ABR64138	Abf64138 Aspergill
836	4	66.7	404	4	ABG12109	Abg12109 Novel hum	909	4	66.7	469	6	ABR64155	Abf64155 Aspergill
837	4	66.7	404	5	ABP66007	Abp66007 Bifidobac	910	4	66.7	469	6	ABR64169	Abf64169 Aspergill
838	4	66.7	404	7	ADB80207	Adb80207 Mycobacte	911	4	66.7	469	6	ABR64164	Abf64164 Aspergill
839	4	66.7	404	7	ADE10273	Adel0273 S. lavend	912	4	66.7	469	6	ABR64141	Abf64141 Aspergill
840	4	66.7	405	3	AAY32310	Aay32310 Soybean a	913	4	66.7	469	6	ABR64128	Abf64128 Wild type
841	4	66.7	406	6	ABO0622	Abo0622 Novel hum	914	4	66.7	469	6	ABR64172	Abf64172 Aspergill
842	4	66.7	410	3	AAY32307	Aay32307 Rice acid	915	4	66.7	469	6	ABR64135	Abf64135 Aspergill
843	4	66.7	410	4	AAE00849	Aae00849 Human nov	916	4	66.7	469	6	ABR64165	Abf64165 Aspergill
844	4	66.7	411	4	AAU54878	Aau54878 Propionib	917	4	66.7	469	6	ABR64167	Abf64167 Aspergill
845	4	66.7	411	6	ABM51397	Abm51397 Propionib	918	4	66.7	469	6	ABR64175	Abf64175 Aspergill
846	4	66.7	414	4	AAE00845	Aae00845 Human nov	919	4	66.7	469	6	ABR64145	Abf64145 Aspergill
847	4	66.7	417	4	ABB67072	Abb67072 Drosophil	920	4	66.7	469	6	ABR64133	Abf64133 Aspergill
848	4	66.7	417	4	ABB67073	Abb67073 Drosophil	921	4	66.7	469	6	ABR64158	Abf64158 Aspergill
849	4	66.7	417	4	ABB62824	Abb62824 Drosophil	922	4	66.7	469	6	ABR64174	Abf64174 Aspergill
850	4	66.7	418	4	ABG14153	Abg14153 Novel hum	923	4	66.7	469	6	ABR64131	Abf64131 Aspergill
851	4	66.7	418	4	ABG03637	Abg03637 Novel hum	924	4	66.7	469	6	ABR64137	Abf64137 Aspergill
852	4	66.7	418	4	ABG07575	Abg07575 Novel hum	925	4	66.7	469	6	ABR64162	Abf64162 Aspergill
853	4	66.7	418	4	ABG07713	Abg07713 Novel hum	926	4	66.7	469	6	ABR64146	Abf64146 Aspergill
854	4	66.7	420	3	AAY32428	Aay32428 Plant ret	927	4	66.7	469	6	ABR64163	Abf64163 Aspergill
855	4	66.7	423	5	ABP99400	Abp99400 Arabidops	928	4	66.7	469	6	ABR64136	Abf64136 Aspergill
856	4	66.7	425	4	ABG27494	Abg27494 Novel hum	929	4	66.7	469	6	ABR64143	Abf64143 Aspergill
857	4	66.7	425	4	ABG08503	Abg08503 Novel hum	930	4	66.7	469	6	ABR64154	Abf64154 Aspergill
858	4	66.7	426	4	AAB70789	Aab70789 N. magada	931	4	66.7	470	6	ABR64166	Abf64166 Aspergill
859	4	66.7	429	4	AAB95767	Aab95767 Human pro	932	4	66.7	470	6	ABU24443	Abu24443 Protein e
860	4	66.7	429	7	ADB74319	Adb74319 Mycobacte	933	4	66.7	474	2	AAR80507	Aar80507 S. livida
861	4	66.7	432	4	ABG19159	Abg19159 Novel hum	934	4	66.7	474	7	ADB74569	Adb74569 Mycobacte
862	4	66.7	433	2	AAW36029	Aaw36029 Protein e	935	4	66.7	476	6	ABU47353	Abu47353 Protein e
863	4	66.7	433	2	AAW71060	Aaw71060 Multiple	936	4	66.7	477	4	AAB81181	Aab81181 Transglut
864	4	66.7	433	5	ABP65809	Abp65809 Bifidobac	937	4	66.7	477	6	ABU07392	Abu07392 Foreign p
865	4	66.7	433	7	ADB84376	Adb84376 MSRV-1 as	938	4	66.7	480	6	ABR64129	Abf64129 Aspergill
866	4	66.7	434	6	ABU41213	Abu41213 Protein e	939	4	66.7	480	7	ADE81195	Ade81195 Orfil, SE
867	4	66.7	439	4	AAE00240	Aae00240 Taxus cus	940	4	66.7	481	4	ABG29555	Abg29555 Novel hum
868	4	66.7	439	5	ABB79398	Abb79398 Taxane sy	941	4	66.7	482	6	ABR64130	Abf64130 Aspergill
869	4	66.7	439	6	ABB82996	Abb82996 T. cuspid	942	4	66.7	483	2	AAW82550	Aaw82550 Human LIR
870	4	66.7	439	7	ADB91939	Adb91939 Acyltrans	943	4	66.7	483	3	AAB04175	Aab04175 Leukocyte
871	4	66.7	440	4	AAU69493	Aau69493 Human pur	944	4	66.7	483	7	ABR44282	Abf44282 Human leu
872	4	66.7	441	5	ABB91785	Abb91785 Herbicida	945	4	66.7	484	4	AAU34864	Aau34864 E. coli c
873	4	66.7	444	4	AAB81163	Aab81163 Transglut	946	4	66.7	484	6	ABU28873	Abu28873 Protein e
874	4	66.7	445	7	ADD47439	Add47439 Rat Prote	947	4	66.7	489	6	ABU09066	Abu09066 Mycobacte
875	4	66.7	447	6	ABU19837	Abu19837 Protein e	948	4	66.7	489	6	ABU09068	Abu09068 Mycobacte
876	4	66.7	449	6	ABM15831	Abm15831 Mycobacte	949	4	66.7	489	6	ABU09069	Abu09069 Mycobacte
877	4	66.7	451	4	AAE00844	Aae00844 Human nov	950	4	66.7	489	6	ABU09062	Abu09062 Mycobacte
878	4	66.7	452	5	ABB92178	Abb92178 Herbicida	951	4	66.7	489	6	ABU09067	Abu09067 Mycobacte
879	4	66.7	452	7	ADC01384	Adc01384 Enterohae	952	4	66.7	489	6	ABU09063	Abu09063 Mycobacte
880	4	66.7	453	4	ABBS8304	Abbs8304 Drosophil	953	4	66.7	489	6	ABU09064	Abu09064 Mycobacte
881	4	66.7	457	4	AAU61200	Aau61200 Propionib	954	4	66.7	489	6	ABU09065	Abu09065 Mycobacte
882	4	66.7	457	6	ABM57719	Abm57719 Propionib	955	4	66.7	491	4	AAB95343	Aab95343 Human pro
883	4	66.7	461	6	ABU24727	Abu24727 Protein e	956	4	66.7	494	7	ADC61151	Adc61151 Baeyer-Vi
884	4	66.7	464	4	AAE00843	Aae00843 Human nov	957	4	66.7	495	4	AAG62159	Aag62159 Human gen
885	4	66.7	464	5	ABB49506	Abb49506 Listeria	958	4	66.7	495	5	ABG63555	Abg63555 Human alb
886	4	66.7	464	6	ABU32474	Abu32474 Protein e	959	4	66.7	495	6	ABU40304	Abu40304 Protein e
887	4	66.7	464	6	ABU25468	Abu25468 Protein e	960	4	66.7	497	4	ABG03007	Abg03007 Novel hum
888	4	66.7	466	5	AAU79040	Aau79040 Human imm	961	4	66.7	497	6	ABP76773	Abp76773 N. gonorr
889	4	66.7	468	4	ABB71291	Abb71291 Drosophil	962	4	66.7	498	5	ABP43865	Abp43865 Human mRN
890	4	66.7	469	5	ABP35645	Abp35645 Fungal ZB	963	4	66.7	498	7	ABU61938	Abu61938 Human ful
891	4	66.7	469	6	ABR64171	Abf64171 Aspergill	964	4	66.7	501	4	AAB68273	Aab68273 Amino aci
892	4	66.7	469	6	ABR64132	Abf64132 Aspergill	965	4	66.7	503	3	AAV96751	Aav96751 A. terreu
893	4	66.7	469	6	ABR64142	Abf64142 Aspergill	966	4	66.7	503	5	ABP35644	Abp35644 Fungal ZB
894	4	66.7	469	6	ABR64144	Abf64144 Aspergill	967	4	66.7	512	4	ABG07679	Abg07679 Novel hum
895	4	66.7	469	6	ABR64147	Abf64147 Aspergill	968	4	66.7	514	2	AAW69235	Aaw69235 FcR-V pro
896	4	66.7	469	6	ABR64148	Abf64148 Aspergill	969	4	66.7	516	4	AAU46381	Aau46381 Propionib
897	4	66.7	469	6	ABR64152	Abf64152 Aspergill	970	4	66.7	516	6	ABM42900	Abm42900 Propionib
898	4	66.7	469	6	ABR64173	Abf64173 Aspergill	971	4	66.7	517	5	ABB92214	Abb92214 Herbicida
899	4	66.7	469	6	ABR64156	Abf64156 Aspergill	972	4	66.7	518	4	ABG13534	Abg13534 Novel hum
900	4	66.7	469	6	ABR64157	Abf64157 Aspergill	973	4	66.7	519	4	AAG64659	Aag64659 Hydroxyin
901	4	66.7	469	6	ABR64159	Abf64159 Aspergill	974	4	66.7	523	5	ABP67995	Abp67995 Human col

975	4	66.7	523	6	ABP78692	Abp78692	N. gonorr
976	4	66.7	523	7	ABU61933	Abu61933	Human Hiw
977	4	66.7	525	4	ABG09393	Abg09393	Novel hum
978	4	66.7	525	4	ABG20264	Abg20264	Novel hum
979	4	66.7	526	2	AAy33686	Aay33686	S. erythr
980	4	66.7	527	6	ABM65307	Abm65307	Propionib
981	4	66.7	535	5	ABP65818	Abp65818	Bifidobac
982	4	66.7	539	3	AAB08667	Aab08667	A human E
983	4	66.7	542	4	ABB71255	Abb71255	Drosophil
984	4	66.7	542	5	ABB92667	Abb92667	Herbicida
985	4	66.7	543	2	AAW36503	Aaw36503	Human hya
986	4	66.7	544	3	AAy57302	Aay57302	G. lampli
987	4	66.7	548	2	AAW72165	Aaw72165	HSV-2 str
988	4	66.7	552	3	AAy84883	Aay84883	A GFP-I-k
989	4	66.7	553	2	AAy37788	Aay37788	Chlamydia
990	4	66.7	553	3	AAy78136	Aay78136	Recombina
991	4	66.7	553	3	AAy78137	Aay78137	Recombina
992	4	66.7	553	3	AAG27820	Aag27820	Arabidops
993	4	66.7	553	5	ABG91038	Abg91038	Chlamydia
994	4	66.7	553	5	ABB94288	Abb94288	Chlamydia
995	4	66.7	553	5	AAU93097	Aau93097	Arabidops
996	4	66.7	553	6	ABU49981	Abu49981	Protein e
997	4	66.7	553	7	ADD43830	Add43830	Chlamydia
998	4	66.7	553	7	ADE37177	Ade37177	Plant yie
999	4	66.7	554	5	AAE20293	Aae20293	Chlamydia
1000	4	66.7	554	5	AAE20299	Aae20299	Chlamydia

ALIGNMENTS

RESULT 1	
AAM48538	
ID	AAM48538 standard; peptide; 6 AA.
XX	
AC	AAM48538;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 41.
XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US014346.
XX	
PR	02-MAY-2000; 2000US-0201261P.
PR	22-AUG-2000; 2000US-00643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYYA) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation domain
PT	fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT	activation, and for treating asthma, lung inflammation, psoriasis.
XX	

PS	Claim 6; Page 61; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC	AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC	residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC	antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC	antirheumatic, antiarthritic, osteopathic, antibacterial,
CC	immunosuppressive, dermatological, neuroprotective, nootropic,
CC	antiatherosclerotic, virucide and antiallergic activity. The compounds
CC	act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC	blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC	domain that results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC	for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC	cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC	bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC	lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC	transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC	viral infections; and ataxia telangiectasia. The compounds are also
CC	useful for treating pro-inflammatory responses such as allergies,
CC	urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC	sunburn, aging and arthritis
XX	
SQ	Sequence 6 AA;
	Query Match 100.0%; Score 6; DB 5; Length 6;
	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ADWSWA 6
Db	
	1 ADWSWA 6
RESULT 2	
AAM48570	
ID	AAM48570 standard; peptide; 6 AA.
XX	
AC	AAM48570;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 73.
XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US014346.
XX	
PR	02-MAY-2000; 2000US-0201261P.
PR	22-AUG-2000; 2000US-00643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYYA) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	

PT Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antiinflammatory, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiallergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db |||||
1 ADWSWA 6

RESULT 3
ADA61814
ID ADA61814 standard; peptide; 6 AA.
XX
AC ADA61814;
XX
DT 20-NOV-2003 (first entry)
DE NFkB essential modulator (NEMO) binding peptide #14.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.

OS Unidentified.
XX
XX US2003054999-A1.
PN
XX
PD 20-MAR-2003.
XX
XX 02-MAY-2001; 2001US-00847946.
PF
XX
XX 02-MAY-2000; 2000US-0201261P.
PR
XX

(MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.
DR
XX New compound for diagnosing or treating inflammatory disorders, e.g.
XX asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Claim 6; Page 23; 37pp; English.
PS
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db |||||
1 ADWSWA 6

RESULT 4
ADA61846
ID ADA61846 standard; peptide; 6 AA.
XX
AC ADA61846;
XX
DT 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #46.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.

XX Unidentified.
OS
XX US2003054999-A1.
PN
XX
PD 20-MAR-2003.
XX
XX 02-MAY-2001; 2001US-00847946.
PF
XX
XX 02-MAY-2000; 2000US-0201261P.
PR
XX

(MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX

DR WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.

PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding

PT sequence.

XX Claim 6; Page 23; 37pp; English.

PS The invention describes an anti-inflammatory compound comprising (I). The

XX compound is useful for diagnosing or treating inflammatory disorders,

CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,

CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.

CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence

CC of an anti-inflammatory peptide that binds to, and down-regulates,

CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX Sequence 6 AA;

SQ Query Match 100.0%; Score 6; DB 6; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db |||||

1 ADWSWA 6

RESULT 5

AAM48574

ID AAM48574 standard; peptide; 7 AA.

XX AAM48574;

XX 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 77.

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

OS WO200183554-A2.

XX 08-NOV-2001.

PD 02-MAY-2001; 2001WO-US014346.

PF 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

PR (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV YALE.

PA May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

DR Novel antiinflammatory compound comprising membrane translocation domain

PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB

PT activation, and for treating asthma, lung inflammation, psoriasis.

XX Claim 6; Page 62; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-

CC AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antirheumatic, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,

CC antiatherosclerotic, virucide and antiallergic activity. The compounds

CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

CC domain that results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compounds are useful

CC for treating inflammatory disorders, e.g. asthma, lung inflammation or

CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;

CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;

CC viral infections; and ataxia telangiectasia. The compounds are also

CC useful for treating pro-inflammatory responses such as allergies,

CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,

CC sunburn, aging and arthritis

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 6; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db |||||

1 ADWSWA 6

RESULT 6

ADA61850

ID ADA61850 standard; peptide; 7 AA.

XX ADA61850;

AC 20-NOV-2003 (first entry)

XX NFkB essential modulator (NEMO) binding peptide #50.

DT NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;

XX antinflammatory; antiasthmatic; antipsoriatic; antirheumatic;

DE antiarthritic; osteopathic; antibacterial; immunosuppressive;

XX dermatological; neuroprotective; cytostatic; nootropic; virucide;

KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;

KW psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator.

XX Unidentified.

OS US2003054999-A1.

XX 20-MAR-2003.

PD 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

PR (MAYM/) MAY M J.

XX (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

PI WPI; 2003-596541/56.

XX

XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX Claim 6; Page 23; 37pp; English.
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 6; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWA 6
Db 1 ADWSWA 6
RESULT 7
AAM48575
ID AAM48575 standard; peptide; 8 AA.
XX
AC AAM48575;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 78.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014346.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiallergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 6; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWA 6
Db 1 ADWSWA 6
RESULT 8
AAM48567
ID AAM48567 standard; peptide; 8 AA.
XX
AC AAM48567;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 70.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014346.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.

XX PS Claim 6; Page 62; 88pp; English.

XX CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-

CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antiinflammatory, antiarthritic, osteopathic, antibacterial,

CC antirheumatic, dermatological, neuroprotective, nootropic,

CC immunosuppressive, antidiabetic and antiallergic activity. The compounds

CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

CC domain that results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compounds are useful

CC for treating inflammatory disorders, e.g. asthma, lung inflammation or

CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;

CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;

CC viral infections; and ataxia telangiectasia. The compounds are also

CC useful for treating pro-inflammatory responses such as allergies,

CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,

CC sunburn, aging and arthritis

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 6; DB 5; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db |||||

3 ADWSWA 8

RESULT 9

ADA61851

ID ADA61851 standard; peptide; 8 AA.

XX AC ADA61851;

XX DT 20-NOV-2003 (first entry)

XX NFkB essential modulator (NEMO) binding peptide #51.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;

KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;

KW antiarthritic; osteopathic; antibacterial; immunosuppressive;

KW dermatological; neuroprotective; cytostatic; nootropic; virucide;

KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;

KW psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator.

XX OS Unidentified.

XX PN US2003054999-A1.

XX PD 20-MAR-2003.

XX PF 02-MAY-2001; 2001US-00847946.

XX PR 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

XX

PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.

PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding

PT sequence.

XX Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The

CC compound is useful for diagnosing or treating inflammatory disorders,

CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,

CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.

CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence

CC of an anti-inflammatory peptide that binds to, and down-regulates,

CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 6; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db |||||

1 ADWSWA 6

RESULT 10

ADA61843

ID ADA61843 standard; peptide; 8 AA.

XX AC ADA61843;

XX DT 20-NOV-2003 (first entry)

XX NFkB essential modulator (NEMO) binding peptide #43.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;

KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;

KW antiarthritic; osteopathic; antibacterial; immunosuppressive;

KW dermatological; neuroprotective; cytostatic; nootropic; virucide;

KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;

KW psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator.

XX OS Unidentified.

XX PN US2003054999-A1.

XX PD 20-MAR-2003.

XX PF 02-MAY-2001; 2001US-00847946.

XX PR 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.

PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
PS Claim 6; Page 23; 37pp; English.
XX
CC The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 6; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 3 ADWSWA 8

RESULT 11
AAM48573
ID AAM48573 standard; peptide; 9 AA.
XX
AC AAM48573;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 76.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014346.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiallergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 6; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 2 ADWSWA 7

RESULT 12
AAM48566
ID AAM48566 standard; peptide; 9 AA.
XX
AC AAM48566;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 69.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014346.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
PS Claim 6; Page 62; 88pp; English.

Mon Jul 26 09:11:20 2004

fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 9 AA;

Query Match 100.0%; Score 6; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 |||||
Db 1 ADWSWA 6

RESULT 14

AAM48572
ID AAM48572 standard; peptide; 9 AA.

XX AAM48572;

XX 20-MAR-2002 (first entry)

DT Anti-inflammatory peptide SEQ ID NO 75.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
DE antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

PF 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

PI

XX The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 9 AA;

Query Match 100.0%; Score 6; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 |||||
Db 1 ADWSWA 6

RESULT 13

AAM48569
ID AAM48569 standard; peptide; 9 AA.

XX AAM48569;

XX 20-MAR-2002 (first entry)

DT Anti-inflammatory peptide SEQ ID NO 72.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

PF 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain

PT

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain

PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB

PT activation, and for treating asthma, lung inflammation, psoriasis.

XX Claim 6; Page 62; 88pp; English.

PS

XX The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-

CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antirheumatic, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,

CC antiatherosclerotic, virucide and antiallergic activity. The compounds

CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

CC domain that results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compounds are useful

CC for treating inflammatory disorders, e.g. asthma, lung inflammation or

CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;

CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;

CC viral infections; and ataxia telangiectasia. The compounds are also

CC useful for treating pro-inflammatory responses such as allergies,

CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,

CC sunburn, aging and arthritis

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 6; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db 3 ADWSWA 8

RESULT 15

ADA61848

ID ADA61848 standard; peptide; 9 AA.

XX

AC ADA61848;

XX

DT 20-NOV-2003 (first entry)

XX

DE NFkB essential modulator (NEMO) binding peptide #48.

XX

KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;

KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;

KW antiarthritic; osteopathic; antibacterial; immunosuppressive;

KW dermatological; neuroprotective; cytostatic; nootropic; virucide;

KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;

KW psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator.

XX

OS Unidentified.

XX

PN US2003054999-A1.

XX

PD 20-MAR-2003.

XX

PF 02-MAY-2001; 2001US-00847946.

XX

PR 02-MAY-2000; 2000US-0201261P.

XX

PA (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

XX

PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX

DR WPI; 2003-596541/56.

XX

PT New compound for diagnosing or treating inflammatory disorders, e.g.

PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding

PT sequence.

XX

PS Claim 6; Page 23; 37pp; English.

XX

CC The invention describes an anti-inflammatory compound comprising (I). The

CC compound is useful for diagnosing or treating inflammatory disorders,

CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,

CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.

CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence

CC of an anti-inflammatory peptide that binds to, and down-regulates,

CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 6; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db 3 ADWSWA 8

RESULT 16

ADA61841

ID ADA61841 standard; peptide; 9 AA.

XX

AC ADA61841;

XX

DT 20-NOV-2003 (first entry)

XX

DE NFkB essential modulator (NEMO) binding peptide #41.

XX

KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;

KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;

KW antiarthritic; osteopathic; antibacterial; immunosuppressive;

KW dermatological; neuroprotective; cytostatic; nootropic; virucide;

KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;

KW psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator.

XX

OS Unidentified.

XX

PN US2003054999-A1.

XX

PD 20-MAR-2003.

XX

PF 02-MAY-2001; 2001US-00847946.

XX

PR 02-MAY-2000; 2000US-0201261P.

XX

PA (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

Mon Jul 26 09:11:20 2004

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR

XX New compound for diagnosing or treating inflammatory disorders, e.g.
XX asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Claim 6; Page 23; 37pp; English.
PS
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db | | | | |
1 ADWSWA 6

RESULT 17
ADA61849
ID ADA61849 standard; peptide; 9 AA.
XX
AC ADA61849;
XX
XX 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #49.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.

XX Unidentified.
OS
XX US2003054999-A1.
XX
XX 20-MAR-2003.
XX
XX 02-MAY-2001; 2001US-00847946.
PF
XX 02-MAY-2000; 2000US-0201261P.
PR
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR
XX

PT New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Claim 6; Page 23; 37pp; English.
PS
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db | | | | |
2 ADWSWA 7

RESULT 18
ADA61845
ID ADA61845 standard; peptide; 9 AA.
XX
AC ADA61845;
XX
XX 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #45.

XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.

XX Unidentified.
OS
XX US2003054999-A1.
XX
XX 20-MAR-2003.
XX
XX 02-MAY-2001; 2001US-00847946.
PF
XX 02-MAY-2000; 2000US-0201261P.
PR
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX

PS Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence of an anti-inflammatory peptide that binds to, and down-regulates, necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX Sequence 9 AA;

Query Match 100.0%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
|||||

Db 1 ADWSWA 6

RESULT 19

ADA61842

ID ADA61842 standard; peptide; 9 AA.

XX

AC ADA61842;

XX

DT 20-NOV-2003 (first entry)

XX

DE NFkB essential modulator (NEMO) binding peptide #42.

XX

KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antibacterial; immunosuppressive; dermatological; neuroprotective; cytostatic; nootropic; virucide; gene therapy; anti-inflammatory; inflammatory disorder; asthma; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; sepsis; vasculitis; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis; Alzheimer's disease; viral infection; NF-kappa B essential modulator; necrosis factor kappa B essential modulator.

XX

OS Unidentified.

XX

PN US2003054999-A1.

XX

PD 20-MAR-2003.

XX

PF 02-MAY-2001; 2001US-00847946.

XX

PR 02-MAY-2000; 2000US-0201261P.

XX

PA (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

XX

PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX

DR WPI; 2003-596541/56.

XX

PT New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.

XX

PS Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,

CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence of an anti-inflammatory peptide that binds to, and down-regulates, necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX Sequence 9 AA;

Query Match 100.0%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
|||||

Db 1 ADWSWA 6

RESULT 20

AAM48568

ID AAM48568 standard; peptide; 10 AA.

XX

AC AAM48568;

XX

DT 20-MAR-2002 (first entry)

XX

DE Anti-inflammatory peptide SEQ ID NO 71.

XX

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX

OS Synthetic.

XX

PN WO200183554-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US014346.

XX

PR 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX

PA (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX

PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX

DR WPI; 2002-121889/16.

XX

PT Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.

XX

PS Claim 6; Page 62; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful

act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, autoimmune diseases such as bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 6; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 3 ADWSWA 8

RESULT 21
AAM48571
ID AAM48571 standard; peptide; 10 AA.
XX AAM48571;
AC AAM48571;
XX 20-MAR-2002 (first entry)
DT Anti-inflammatory peptide SEQ ID NO 74.
DE
XX
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
OS
XX WO200183554-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US014346.
PF
XX
XX 02-MAY-2000; 2000US-0201261P.
PR
XX 22-AUG-2000; 2000US-00643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
PI WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.
PT
PT
XX Claim 6; Page 62; 88pp; English.
PS
XX The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds

for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 6; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 2 ADWSWA 7

RESULT 21
AAM48571
ID AAM48571 standard; peptide; 10 AA.
XX AAM48571;
AC AAM48571;
XX 20-MAR-2002 (first entry)
DT Anti-inflammatory peptide SEQ ID NO 74.
DE
XX
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
OS
XX WO200183554-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US014346.
PF
XX
XX 02-MAY-2000; 2000US-0201261P.
PR
XX 22-AUG-2000; 2000US-00643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
PI WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.
PT
PT
XX Claim 6; Page 62; 88pp; English.
PS
XX The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds

CC The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 2 ADWSWA 7
| | | | |

RESULT 23
ADA61847
ID ADA61847 standard; peptide; 10 AA.
XX
AC ADA61847;
XX
DT 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #47.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
OS Unidentified.
XX
PN US2003054999-A1.
XX
XX 20-MAR-2003.
PD
XX 02-MAY-2001; 2001US-00847946.
PF
XX 02-MAY-2000; 2000US-0201261P.
PR
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX
XX WPI; 2003-596541/56.
DR
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
PS Claim 6; Page 23; 37pp; English.
XX
CC The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 3 ADWSWA 8
| | | | |

RESULT 24
AAM48565
ID AAM48565 standard; peptide; 11 AA.
XX
AC AAM48565;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 68.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014346.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
XX WPI; 2002-121889/16.
DR
XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiallergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC and chronic inflammation, by down-regulating the expression of E-selectin
CC on leukocytes or by blocking osteoclast differentiation. The compound is
CC useful in treating NF-kB mediated conditions, where the condition is an
CC inflammatory disorder, an autoimmune disease, transplant rejection,
CC osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
CC infection or ataxia telangiectasia. The inflammatory disorder is asthma,
CC allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
CC psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
CC inflammatory bowel disease, chronic obstructive pulmonary disease,
CC vasculitis and bursitis. The inflammatory disorder may also be
CC dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
CC and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta

SQ Sequence 6 AA;

Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
DB 1 ADWSW 5

RESULT 27

ABB08728

ID ABB08728 standard; peptide; 6 AA.

XX ABB08728;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 5.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neutropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 6 /note= "wildtype Leu substituted by Ala"

XX WO200183547-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US040654.

PF 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain.

XX Claim 23; Page 44; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound (ABB08725-
CC ABB08742) comprising at least one NEMO binding domain (ABB77313). The
CC compound has acts through selective inhibition of cytokine-mediated NF-kB
CC activation by blocking the interaction of NEMO with IKKbeta at the NEMO
CC binding domain. Blockage of IKKbeta-NEMO interaction results in
CC inhibition of IKKbeta kinase activation and subsequent decreased
CC phosphorylation of IkappaB. The compound may also act (directly or
CC indirectly) by blocking the recruitment of leukocytes into sites of acute
CC and chronic inflammation, by down-regulating the expression of E-selectin
CC on leukocytes or by blocking osteoclast differentiation. The compound is
CC useful in treating NF-kB mediated conditions, where the condition is an
CC inflammatory disorder, an autoimmune disease, transplant rejection,
CC osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
CC infection or ataxia telangiectasia. The inflammatory disorder is asthma,
CC allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
CC psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
CC inflammatory bowel disease, chronic obstructive pulmonary disease,
CC vasculitis and bursitis. The inflammatory disorder may also be
CC dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
CC and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta

XX Sequence 6 AA;

Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 2 DWSWA 6

RESULT 28

AAM48537

ID AAM48537 standard; peptide; 6 AA.

XX AAM48537;

XX 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 40.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

XX DE Anti-inflammatory peptide SEQ ID NO 62.

XX DE

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US014346.

XX PR 02-MAY-2000; 2000US-0201261P.

XX PR 22-AUG-2000; 2000US-00643260.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX PT Novel antiinflammatory compound comprising membrane translocation domain

PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB

PT activation, and for treating asthma, lung inflammation, psoriasis.

XX

PS Claim 6; Page 62; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-

CC AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antirheumatic, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,

CC antiatherosclerotic, virucide and antiallergic activity. The compounds

CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

CC domain that results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compounds are useful

CC for treating inflammatory disorders, e.g. asthma, lung inflammation or

CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;

CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;

CC viral infections; and ataxia telangiectasia. The compounds are also

CC useful for treating pro-inflammatory responses such as allergies,

CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,

CC sunburn, aging and arthritis

XX

SQ Sequence 6 AA;

Query Match 83.3%; Score 5; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6

DB 2 DWSWA 6

RESULT 31

AAM48509

ID AAM48509 standard; peptide; 6 AA.

XX AAM48509;

XX AC

DT 20-MAR-2002 (first entry)

XX

DE NBD mutant peptide SEQ ID NO 4.

XX

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX

OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US014346.

XX PR 02-MAY-2000; 2000US-0201261P.

XX PR 22-AUG-2000; 2000US-00643260.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX

PT Novel antiinflammatory compound comprising membrane translocation domain

PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB

PT activation, and for treating asthma, lung inflammation, psoriasis.

XX

PS Example 6; Page 47; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-

CC AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antirheumatic, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,

CC antiatherosclerotic, virucide and antiallergic activity. The compounds

CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

CC domain that results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compounds are useful

CC for treating inflammatory disorders, e.g. asthma, lung inflammation or

CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;

CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;

CC viral infections; and ataxia telangiectasia. The compounds are also

CC useful for treating pro-inflammatory responses such as allergies,

CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,

CC sunburn, aging and arthritis

XX

SQ Sequence 6 AA;

Query Match 83.3%; Score 5; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

DB 1 ADWSW 5

Mon Jul 26 09:11:20 2004

QY	2	DWSWA 6
Db	2	DWSWA 6
RESULT 33		
AAM48536		
ID	AAM48536	standard; peptide; 6 AA.
XX		
AC	AAM48536;	
XX		
DT	20-MAR-2002	(first entry)
DE	Anti-inflammatory peptide SEQ ID NO 39.	
XX		
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;	
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;	
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;	
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
KW	cytokine; NfkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KW	autoimmune disorder; multiple sclerosis; transplant rejection;	
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
XX		
OS	Synthetic.	
XX		
PN	WO200183554-A2.	
XX		
PD	08-NOV-2001.	
XX		
PF	02-MAY-2001; 2001WO-US014346.	
XX		
PR	02-MAY-2000; 2000US-0201261P.	
PR	22-AUG-2000; 2000US-00643260.	
XX		
PA	(PRAE-) PRAECIS PHARM INC.	
PA	(UYVA) UNIV YALE.	
XX		
PI	May MJ, Ghosh S, Findeis MA, Phillips K;	
XX		
DR	WPI; 2002-121889/16.	
XX		
PT	Novel antiinflammatory compound comprising membrane translocation domain	
PT	fused to NEMO binding sequence, useful for blocking nuclear factor kappaB	
PT	activation, and for treating asthma, lung inflammation, psoriasis.	
XX		
PS	Claim 6; Page 61; 88pp; English.	
XX		
CC	The invention relates to an antiinflammatory compound (especially	
CC	AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-	
CC	AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid	
CC	residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The	
CC	antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,	
CC	antirheumatic, antiarthritic, osteopathic, antibacterial,	
CC	immunosuppressive, dermatological, neuroprotective, nootropic,	
CC	antiatherosclerotic, virucide and antiallergic activity. The compounds	
CC	act as selective inhibitors of cytokine-mediated NfkappaB activation by	
CC	blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding	
CC	domain that results in inhibition of IKKbeta kinase activation and	
CC	subsequent decreased phosphorylation of IkappaB. The compounds are useful	
CC	for treating inflammatory disorders, e.g. asthma, lung inflammation or	
CC	cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory	
CC	bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as	
CC	lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;	
CC	transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;	
CC	viral infections; and ataxia telangiectasia. The compounds are also	
CC	useful for treating pro-inflammatory responses such as allergies,	
CC	urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,	
XX		
SQ	Sequence 6 AA;	

RESULT 32		
AAM48510		
ID	AAM48510	standard; peptide; 6 AA.
XX		
AC	AAM48510;	
XX		
DT	20-MAR-2002	(first entry)
XX		
DE	NBD mutant peptide SEQ ID NO 5.	
XX		
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;	
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;	
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;	
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
KW	cytokine; NfkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KW	autoimmune disorder; multiple sclerosis; transplant rejection;	
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
XX		
OS	Synthetic.	
XX		
PN	WO200183554-A2.	
XX		
PD	08-NOV-2001.	
XX		
PF	02-MAY-2001; 2001WO-US014346.	
XX		
PR	02-MAY-2000; 2000US-0201261P.	
PR	22-AUG-2000; 2000US-00643260.	
XX		
PA	(PRAE-) PRAECIS PHARM INC.	
PA	(UYVA) UNIV YALE.	
XX		
PI	May MJ, Ghosh S, Findeis MA, Phillips K;	
XX		
DR	WPI; 2002-121889/16.	
XX		
PT	Novel antiinflammatory compound comprising membrane translocation domain	
PT	fused to NEMO binding sequence, useful for blocking nuclear factor kappaB	
PT	activation, and for treating asthma, lung inflammation, psoriasis.	
XX		
PS	Example 6; Page 47; 88pp; English.	
XX		
CC	The invention relates to an antiinflammatory compound (especially	
CC	AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-	
CC	AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid	
CC	residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The	
CC	antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,	
CC	antirheumatic, antiarthritic, osteopathic, antibacterial,	
CC	immunosuppressive, dermatological, neuroprotective, nootropic,	
CC	antiatherosclerotic, virucide and antiallergic activity. The compounds	
CC	act as selective inhibitors of cytokine-mediated NfkappaB activation by	
CC	blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding	
CC	domain that results in inhibition of IKKbeta kinase activation and	
CC	subsequent decreased phosphorylation of IkappaB. The compounds are useful	
CC	for treating inflammatory disorders, e.g. asthma, lung inflammation or	
CC	cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory	
CC	bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as	
CC	lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;	
CC	transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;	
CC	viral infections; and ataxia telangiectasia. The compounds are also	
CC	useful for treating pro-inflammatory responses such as allergies,	
CC	urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,	
XX		
SQ	Sequence 6 AA;	

Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|
|
|
|
|
Db 1 ADWSW 5

RESULT 34
ABU08420
ID ABU08420 standard; peptide; 6 AA.
XX
AC ABU08420;
XX
DT 12-JUN-2003 (first.entry)
XX
DE Human NEMO binding site (NBD) mutant peptide #3.
XX
KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW nuclear factor-kappaB induction; inflammatory disorder;
KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW atherosclerosis; viral infection; Ataxia telangiectasia;
KW transplantation detection; immunosuppressive; osteopathic; cytostatic;
KW neutropic; neuroprotective; antiatherosclerotic; virucide; vasotropic;
KW antirheumatic; antiarthritic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002156000-A1.
XX
PD 24-OCT-2002.
XX
PF 02-MAY-2001; 2001US-00847940.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2003-209142/20.
XX
PT Novel antiinflammatory peptide compounds comprising NEMO binding domain,
PT useful for modulating NF-kappaB induction in a cell and for treating NF-
PT kappaB-mediated inflammation disorders e.g., asthma, psoriasis,
PT vasculitis.
XX
PS Claim 22; Page 17; 47pp; English.
XX
CC The present invention relates to antiinflammatory compounds comprising
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are found on
CC IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha)
CC proteins. The antiinflammatory compounds of the invention are useful for
CC modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where
CC the compounds are capable of blocking the interaction between one or more
CC IKKs such as IKKalpha or IKKbeta, and NEMO. The antiinflammatory compound
CC further comprises at least one membrane translocation domain. The
CC compounds are useful for treating inflammatory disorders, autoimmune
CC diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis,
CC viral infections, Ataxia telangiectasia, and for transplantation
CC detection. The compounds of the invention block NF-kappaB induction by
CC IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432
CC represent human NBD mutant peptides
XX
SQ Sequence 6 AA;

Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|
|
|
|
|
Db 1 ADWSW 5

RESULT 35
ABU08421
ID ABU08421 standard; peptide; 6 AA.
XX
AC ABU08421;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human NEMO binding site (NBD) mutant peptide #4.
XX
KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW nuclear factor-kappaB induction; inflammatory disorder;
KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW atherosclerosis; viral infection; Ataxia telangiectasia;
KW transplantation detection; immunosuppressive; osteopathic; cytostatic;
KW neutropic; neuroprotective; antiatherosclerotic; virucide; vasotropic;
KW antirheumatic; antiarthritic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002156000-A1.
XX
PD 24-OCT-2002.
XX
PF 02-MAY-2001; 2001US-00847940.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2003-209142/20.
XX
PT Novel antiinflammatory peptide compounds comprising NEMO binding domain,
PT useful for modulating NF-kappaB induction in a cell and for treating NF-
PT kappaB-mediated inflammation disorders e.g., asthma, psoriasis,
PT vasculitis.
XX
PS Claim 22; Page 17; 47pp; English.
XX
CC The present invention relates to antiinflammatory compounds comprising
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are found on
CC IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha)
CC proteins. The antiinflammatory compounds of the invention are useful for
CC modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where
CC the compounds are capable of blocking the interaction between one or more
CC IKKs such as IKKalpha or IKKbeta, and NEMO. The antiinflammatory compound
CC further comprises at least one membrane translocation domain. The
CC compounds are useful for treating inflammatory disorders, autoimmune
CC diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis,
CC viral infections, Ataxia telangiectasia, and for transplantation
CC detection. The compounds of the invention block NF-kappaB induction by
CC IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432
CC represent human NBD mutant peptides
XX
SQ Sequence 6 AA;

Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Jul 26 09:11:20 2004

QY 2 DWSWA 6
Db 2 DWSWA 6

RESULT 36
ADA61778
ID ADA61778 standard; peptide; 6 AA.
XX AC ADA61778;
XX DT 20-NOV-2003 (first entry)
XX DE IKKbeta NEMO binding domain (NBD) mutant #3.
XX KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator; mutant; mutein.
XX OS Synthetic.
OS Homo sapiens.
XX PN US2003054999-A1.
XX PD 20-MAR-2003.
XX PF 02-MAY-2001; 2001US-00847946.
XX PR 02-MAY-2000; 2000US-0201261P.
XX PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX Example 4; Page 19; 37pp; English.
PS The invention describes an anti-inflammatory compound comprising (I). The
XX compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of a I kappa B kinase beta (IKKbeta) NEMO binding domain (NBD) mutant
CC used in to determine which residues in the NBD are important for binding
CC NEMO (necrosis factor kappa B essential modulator).
XX SQ Sequence 6 AA;
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 1 ADWSW 5

RESULT 38
ADA61811
ID ADA61811 standard; peptide; 6 AA.

RESULT 37
ADA61812
ID ADA61812 standard; peptide; 6 AA.
XX AC ADA61812;
XX DT 20-NOV-2003 (first entry)
XX DE NFkB essential modulator (NEMO) binding peptide #12.
XX KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX OS Unidentified.
XX PN US2003054999-A1.
XX PD 20-MAR-2003.
XX PF 02-MAY-2001; 2001US-00847946.
XX PR 02-MAY-2000; 2000US-0201261P.
XX PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX Claim 6; Page 23; 37pp; English.
PS The invention describes an anti-inflammatory compound comprising (I). The
XX compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX SQ Sequence 6 AA;
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 1 ADWSW 5

RESULT 38
ADA61811
ID ADA61811 standard; peptide; 6 AA.

XX ADA61811;
AC
XX
DT 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #11.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
OS Unidentified.
XX
PN US2003054999-A1.
XX
PD 20-MAR-2003.
XX
PF 02-MAY-2001; 2001US-00847946.
XX
PR 02-MAY-2000; 2000US-0201261P.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX
DR WPI; 2003-596541/56.
XX
PT New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
PS Claim 6; Page 23; 37pp; English.
XX
CC The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 6 AA;

Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 1 ADWSW 5

RESULT 39
ADA61813
ID ADA61813 standard; peptide; 6 AA.
XX
AC ADA61813;
XX
DT 20-NOV-2003 (first entry)
XX

DE NFkB essential modulator (NEMO) binding peptide #13.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
OS Unidentified.
XX
PN US2003054999-A1.
XX
PD 20-MAR-2003.
XX
PF 02-MAY-2001; 2001US-00847946.
XX
PR 02-MAY-2000; 2000US-0201261P.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX
DR WPI; 2003-596541/56.
XX
PT New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
PS Claim 6; Page 23; 37pp; English.
XX
CC The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 6 AA;

Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 2 DWSWA 6

RESULT 40
ADA61835
ID ADA61835 standard; peptide; 6 AA.
XX
AC ADA61835;
XX
DT 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #35.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW

Mon Jul 26 09:11:20 2004

KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
OS Unidentified.
XX
XX US2003054999-A1.
PN
XX 20-MAR-2003.
PD
XX 02-MAY-2001; 2001US-00847946.
PF
XX 02-MAY-2000; 2000US-0201261P.
PR
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR
XX New compound for diagnosing or treating inflammatory disorders, e.g.
XX asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
PT
XX Claim 6; Page 23; 37pp; English.
PS
XX The invention describes an anti-inflammatory compound comprising (I). The
XX compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 6 AA;
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSWA 6
Db |||||
2 DWSWA 6
RESULT 41
ADA61779
ID ADA61779 standard; peptide; 6 AA.
XX
AC ADA61779;
XX
DT 20-NOV-2003 (first entry)
XX
DE IKKbeta NEMO binding domain (NBD) mutant #4.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator; mutant; mutein.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003054999-A1.
XX
XX 20-MAR-2003.
PD
XX 02-MAY-2001; 2001US-00847946.
PF
XX 02-MAY-2000; 2000US-0201261P.
PR
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR
XX New compound for diagnosing or treating inflammatory disorders, e.g.
XX asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
PT
XX Example 4; Page 19; 37pp; English.
PS
XX The invention describes an anti-inflammatory compound comprising (I). The
XX compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of a I kappa B kinase beta (IKKbeta) NEMO binding domain (NBD) mutant
CC used in to determine which residues in the NBD are important for binding
CC NEMO (necrosis factor kappa B essential modulator).
XX
SQ Sequence 6 AA;
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSWA 6
Db |||||
2 DWSWA 6
RESULT 42
ADA61824
ID ADA61824 standard; peptide; 6 AA.
XX
AC ADA61824;
XX
DT 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #24.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.

Mon Jul 26 09:11:20 2004

Alzheimer's disease; viral infection; NF-kappa B essential modulator; necrosis factor kappa B essential modulator.

Unidentified.

US2003054999-A1.

20-MAR-2003.

02-MAY-2001; 2001US-00847946.

02-MAY-2000; 2000US-0201261P.

(MAYM/) MAY M J.

(GHOS/) GHOSH S.

(FIND/) FINDEIS M A.

(PHIL/) PHILLIPS K.

(HANN/) HANNIG G.

May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

WPI; 2003-596541/56.

New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.

Claim 6; Page 23; 37pp; English.

The invention describes an anti-inflammatory compound comprising (I). The compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence of an anti-inflammatory peptide that binds to, and down-regulates, necrosis factor kappa B (NFkB) essential modulator (NEMO).

Sequence 7 AA;

Query Match 83.3%; Score 5; DB 6; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 1 ADWSW 5

RESULT 46

ADA61839

ID ADA61839 standard; peptide; 7 AA.

XX

AC ADA61839;

XX

DT 20-NOV-2003 (first entry)

XX

DE NFkB essential modulator (NEMO) binding peptide #39.

XX

NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antibacterial; immunosuppressive; dermatological; neuroprotective; cytostatic; nootropic; virucide; gene therapy; anti-inflammatory; inflammatory disorder; asthma; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; sepsis; vasculitis; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis; Alzheimer's disease; viral infection; NF-kappa B essential modulator; necrosis factor kappa B essential modulator.

Unidentified.

OS

XX

WO200183554-A2.

08-NOV-2001.

02-MAY-2001; 2001WO-US014346.

02-MAY-2000; 2000US-0201261P.

22-AUG-2000; 2000US-00643260.

(PRAE-) PRAECIS PHARM INC.

(UYYA) UNIV YALE.

May MJ, Ghosh S, Findeis MA, Phillips K;

WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, antirheumatic, antiarthritic, osteopathic, neuroprotective, nootropic, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 7 AA;

Query Match 83.3%; Score 5; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6

Db 2 DWSWA 6

RESULT 45

ADA61828

ID ADA61828 standard; peptide; 7 AA.

XX

AC ADA61828;

XX

DT 20-NOV-2003 (first entry)

XX

DE NFkB essential modulator (NEMO) binding peptide #28.

XX

NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta; antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antibacterial; immunosuppressive; dermatological; neuroprotective; cytostatic; nootropic; virucide; gene therapy; anti-inflammatory; inflammatory disorder; asthma; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; sepsis; vasculitis; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

PN US2003054999-A1.
XX 20-MAR-2003.
PD
XX
PF 02-MAY-2001; 2001US-00847946.
XX
PR 02-MAY-2000; 2000US-0201261P.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.
DR
XX
XX New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.
PT
XX
PS Claim 6; Page 23; 37pp; English.
XX
CC The invention describes an anti-inflammatory compound comprising (I). The compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence of an anti-inflammatory peptide that binds to, and down-regulates, necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 7 AA;

Query Match 83.3%; Score 5; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db |||||
2 DWSWA 6

RESULT 47
AAM48556
ID AAM48556 standard; peptide; 8 AA.
XX
AC AAM48556;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 59.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014346.
XX

PR 02-MAY-2000; 2000US-0201261P.
XX 22-AUG-2000; 2000US-00643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
DR
XX
XX Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.
PT
PT
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis
XX
SQ Sequence 8 AA;

Query Match 83.3%; Score 5; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db |||||
4 DWSWA 8

RESULT 48
AAM48545
ID AAM48545 standard; peptide; 8 AA.
XX
AC AAM48545;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 48.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX

PD	08-NOV-2001.	OS	Synthetic.
XX		XX	
PN	02-MAY-2001; 2001WO-US014346.	PN	WO200183554-A2.
XX		XX	
PD	02-MAY-2000; 2000US-0201261P.	PD	08-NOV-2001.
XX		XX	
PR	22-AUG-2000; 2000US-00643260.	PF	02-MAY-2001; 2001WO-US014346.
XX		XX	
PA	(PRAE-) PRAECIS PHARM INC.	PR	02-MAY-2000; 2000US-0201261P.
PA	(UYVA) UNIV YALE.	PR	22-AUG-2000; 2000US-00643260.
XX		XX	
PI	May MJ, Ghosh S, Findeis MA, Phillips K;	PA	(PRAE-) PRAECIS PHARM INC.
XX		PA	(UYVA) UNIV YALE.
DR	WPI; 2002-121889/16.	XX	
XX		PI	May MJ, Ghosh S, Findeis MA, Phillips K;
XX		XX	WPI; 2002-121889/16.
PT	Novel antiinflammatory compound comprising membrane translocation domain	PT	Novel antiinflammatory compound comprising membrane translocation domain
PT	fused to NEMO binding sequence, useful for blocking nuclear factor kappaB	PT	fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT	activation, and for treating asthma, lung inflammation, psoriasis.	PT	activation, and for treating asthma, lung inflammation, psoriasis.
XX		XX	
PS	Claim 6; Page 62; 88pp; English.	XX	Claim 6; Page 62; 88pp; English.
XX		PS	
CC	The invention relates to an antiinflammatory compound (especially	XX	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-	CC	AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC	AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid	CC	AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC	residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The	CC	residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC	antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,	CC	antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC	antirheumatic, antiarthritic, osteopathic, antibacterial,	CC	antirheumatic, antiarthritic, osteopathic, antibacterial,
CC	immunosuppressive, dermatological, neuroprotective, nootropic,	CC	immunosuppressive, dermatological, neuroprotective, nootropic,
CC	antiatherosclerotic, virucide and antiallergic activity. The compounds	CC	antiatherosclerotic, virucide and antiallergic activity. The compounds
CC	act as selective inhibitors of cytokine-mediated NFkappaB activation by	CC	act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC	blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding	CC	blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC	domain that results in inhibition of IKKbeta kinase activation and	CC	domain that results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of IkappaB. The compounds are useful	CC	subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC	for treating inflammatory disorders, e.g. asthma, lung inflammation or	CC	for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC	cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory	CC	cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC	bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as	CC	bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC	lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;	CC	lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC	transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;	CC	transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC	viral infections; and ataxia telangiectasia. The compounds are also	CC	viral infections; and ataxia telangiectasia. The compounds are also
CC	useful for treating pro-inflammatory responses such as allergies,	CC	useful for treating pro-inflammatory responses such as allergies,
CC	urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,	CC	urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC	sunburn, aging and arthritis	CC	sunburn, aging and arthritis
XX		XX	
SQ	Sequence 8 AA;	SQ	Sequence 8 AA;
	Query Match 83.3%; Score 5; DB 5; Length 8;		Query Match 83.3%; Score 5; DB 5; Length 8;
	Best Local Similarity 100.0%; Pred. No. 1.4e+06;		Best Local Similarity 100.0%; Pred. No. 1.4e+06;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ADWSW 5	QY	2 DWSWA 6
Db	3 ADWSW 7	Db	2 DWSWA 6
	RESULT 49		RESULT 50
	AAM48564		AAM48553
ID	AAM48564 standard; peptide; 8 AA.	ID	AAM48553 standard; peptide; 8 AA.
XX		XX	
AC	AAM48564;	AC	AAM48553;
XX		XX	
DT	20-MAR-2002 (first entry)	DT	20-MAR-2002 (first entry)
XX		XX	
DE	Anti-inflammatory peptide SEQ ID NO 67.	DE	Anti-inflammatory peptide SEQ ID NO 56.
XX		XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;	KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;	KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;	KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;	KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014346.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
XX WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiallergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX
SQ Sequence 8 AA;

Query Match 83.3%; Score 5; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 1 ADWSW 5

Search completed: July 23, 2004, 13:27:11
Job time : 76 secs

THIS PAGE BLANK (USPTO)